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Authors

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Abstract

Campo-Ma'an National Park (CMNP), located within the Guineo-Congolian Rainforest biodiversity hotspot in southern Cameroon, faces intense anthropogenic pressures yet harbors diverse bat assemblages essential for pollination, seed dispersal, and pest control. We conducted the first systematic bat inventory in CMNP, integrating capture-based surveys, acoustic monitoring, and mitochondrial DNA sequencing across 4 habitat types and 4 climatic seasons from August 2023 to February 2025. Over 73 sampling nights (5,256 mist net-hours, 876 harp trap-hours), we captured 625 bats representing 32 species across 20 genera and 6 families (~27% of Cameroon's chiropteran fauna). Notable records include the Data Deficient *Casinycotis campomaanensis* and *Myotis dieteri*, and the Endangered *Pseudoromicia roseveari*. First country records include *Rhinolophus denti* (genetically confirmed) and *M. dieteri*, the latter representing the first documented occurrence within a protected area globally. Potential additional first country records include *R. cf. blasii*, *R. cf. acrotis*, and *Glauconycteris cf. humeralis*. Primary forests supported highest species richness (23 species, $H' = 2.24$), including rare species captured exclusively in this habitat, while farms exhibited highest abundance (31.2%), dominated by frugivorous generalists. The Great Rainy Season yielded greatest diversity (22 species), whereas the Great Dry Season yielded peak abundance (34.72%). Multivariate analyses revealed significant habitat-season effects on assemblage structure. Acoustic characterization of 22 species established the first regional call reference library, with high peak frequency variability in *Hipposideros cf. ruber* ($SD = \pm 41.25$ kHz) suggesting cryptic diversity. Cytochrome-b sequencing corrected ~10% of morphological identifications, confirming *Ps. roseveari* and *R. denti*, while genetic variability in *H. cf. ruber* suggests unresolved cryptic diversity. These results emphasize CMNP's importance for bat conservation amid escalating threats from deforestation and agro-industrial expansion. We recommend preserving primary forests, maintaining habitat corridors, and promoting fruit tree agroforestry in management plans. Future efforts should expand genetic sampling and apply

species distribution modeling to better resolve taxonomic uncertainties and predict habitat suitability.

Keywords: Bat diversity, Campo-Ma'an National Park, habitat associations, habitat-season dynamics, cytochrome b, echolocation, conservation, new records

Introduction

Bats (Mammalia: Chiroptera) represent the second most diverse group of mammals after rodents, accounting for approximately 22% of global mammalian diversity (Burgin et al., 2025). This highly diverse order includes approximately 1,500 species (Simmons & Cirranello, 2025; Torrent et al., 2025) and plays critical roles in tropical ecosystems, particularly in Africa, where around 20% of these species are found (Frick et al., 2020; Monadjem et al., 2024). In the dense tropical forests of Cameroon, bats function as key pollinators, seed dispersers, and natural pest controllers (Bakwo Fils, 2010; Kunz et al., 2011; Monadjem et al., 2024). They occupy a wide range of ecological niches essential for maintaining ecosystem balance (Bakwo Fils, 2009). Despite their ecological significance, bats remain understudied and undervalued in conservation efforts (Bakwo Fils, 2009, 2010) and face threats from habitat loss, climate change, and pervasive human misconceptions and activities (Bakwo Fils, 2009, 2010).

Straddling the Cameroon Volcanic Line, a biodiversity corridor that links the Congo Basin and West African faunal regions, Cameroon is home to a rich chiropteran fauna comprising approximately 118 species (Grunwald et al., 2023, 2025; Van Cakenberghe & Seamark, 2025). More than 50 of these species have been documented in protected forested areas, such as the Dja Biosphere Reserve, Mount Cameroon, Mpem and Djim National Park, and Mbam and Djerem National Park (Bakwo Fils, 2009; Atagana et al., 2018; Mongombe Manga et al., 2020; Atagana et al., 2021; Kingha et al., 2025). However, research remains spatially biased, leaving many biodiverse regions of the country poorly surveyed, including the Campo Ma'an Technical Operational Unit (TOU) and its core protected area, Campo Ma'an National Park (CMNP).

CMNP, located in south Cameroon within the Guineo-Congolian Rainforest biodiversity hotspot (UNESCO, 2018), encompasses a mosaic of habitats, including primary lowland tropical forests, regenerating secondary forests, cocoa and oil palm plantations, savannah patches, village lands, and human settlements. These varied habitats support diverse bat assemblages and species of conservation concern (Bakwo Fils, 2009; CMNP, 2014; Engolo et al., 2024; UNESCO, 2018). The park is home to notable fauna, including critically endangered species such as forest elephants (*Loxodonta cyclotis*) and western lowland gorillas (*Gorilla gorilla gorilla*), as well as the Data Deficient Campo Ma'an fruit bat (*Casinycteris campomaanensis*), which was first described in the park's vicinity (Hassanin, 2014; IUCN, 2025). The evergreen forest core contrasts with peripheral production forests and is characterized by an equatorial climate with two rainy and two dry seasons. Seasonality influences fruit and insect availability and likely affects bat behavior and community dynamics (Klingbeil & Willig, 2010; Bakwo Fils et al., 2014; Forje & Tchamba, 2022).

While CMNP provides economic benefits to local communities through ecotourism and sustainable practices, it faces escalating threats from deforestation, agriculture, logging, hunting, and infrastructure development, including the Kribi Industrial Port Complex, the Memve'ele Hydroelectric Dam and a second planned dam on the Ntem river, agro-industrial

concessions (HEVECAM SA, hevea production; CAMVERT SARL and SOCAPALM, palm oil production), mining exploration (SINOSTEEL Corp), and major transportation projects such as the Kribi-Mbalam railway and the Lolabé-Campo motorway linking trade between Cameroon and Equatorial Guinea (Engolo et al., 2024). These activities jeopardize ecosystems within and around CMNP, particularly habitats that are crucial for bats (Hansen et al., 2013; Forje & Tchamba, 2022; Engolo et al., 2024). Despite research focused on larger mammals in the park (CMNP, 2014; UNESCO, 2018; Engolo et al., 2024), bats have received scant attention, with only a single previous record collected very close to the PA, published by Hassanin (2014). Understanding the composition, diversity, and habitat associations of bats is therefore essential for effective conservation, especially amidst escalating land-use changes (Klingbeil & Willig, 2010; Voigt & Kingston, 2016; Grunwald et al., 2025).

Integrative methodologies that combine morphological, acoustic, and genetic analyses are necessary for clarifying taxonomic uncertainties in morphologically conservative families such as Rhinolophidae and Vespertilionidae, where cryptic species may go unrecognized (Taylor et al., 2019; Patterson et al., 2020; Grunwald et al., 2023, 2025). Systematic inventories are essential for documenting species richness, mapping distributions, and understanding environmental responses, which provide crucial foundational data to enhance knowledge of bat diversity and inform conservation strategies both globally and within Afrotropical areas such as CMNP (Patterson & Webala, 2012; Atagana et al., 2021). Recent studies in Cameroon, such as checklists for Mount Cameroon (Mongombe Manga et al., 2020) and genetic-acoustic surveys in the Mbam Minkom Massif (Grunwald et al., 2023, 2025), underscore the significance of such investigations in understudied areas.

This study aims to provide the first systematic inventory of bats in CMNP. We examined community variation across 4 habitat types (primary forest, secondary forest, farms, human habitats) over an annual seasonal cycle to identify implications for conservation. We employed capture-based surveys, acoustic monitoring, and preliminary cytochrome b (cyt-b) sequencing to enhance species identifications. Specifically, we (i) conducted a species inventory, assessed conservation status, and established a preliminary acoustic reference library; (ii) evaluated seasonal and habitat-specific variation in diversity and abundance; (iii) identified environmental factors influencing distributions through habitat-season interactions; (iv) characterized bat habitat use; and (v) conducted genetic analyses to support taxonomic assignments.

By addressing key knowledge gaps, this research provides a scientific foundation for bat conservation amid increasing anthropogenic pressures in south Cameroon.

Materials and Methods

Study area

This study was conducted in CMNP (2.17-2.75, 9.83-10.80) and surrounding areas within the Technical Operational Unit (TOU), South Cameroon (Figure 1). The CMNP covers 264,064 ha and forms part of the Guineo-Congolian Rainforest, while the broader TOU spans about 771 668 ha, encompassing forest management units (09-021, 09-024 and 09-025), agro-industrial farms, and multi-use zones. Established in 2000, the park is administered across 2 sub-divisions: the Ocean subdivision (including Akom II, Campo, and Nyété districts), and the Ntem valley subdivision (including Ma'an district), each with local wildlife authority stations

(Tchouto et al., 2006; CMNP, 2014; UNESCO, 2018; Forje & Tchamba, 2022; Engolo et al., 2024; Komo Mbarga et al., 2024).

The region's equatorial climate features 4 seasons: a short rainy season (SRS) from March-June, short dry season (SDS) from July-August, a great rainy season (GRS) from September-November, and a great dry season (GDS) from December-February (Suchel, 1987). Annual rainfall averages ~2,800 mm near the coast (around Nyabissan), and ~1,670 mm inland (Tchouto et al., 2006; CMNP, 2014). CMNP lies within the Atlantic basin drainage system and includes the Ntem and Lobé watersheds, with rivers flowing predominantly from northeast to southwest (Mbenoun Masse et al., 2018).

The socio-cultural organization comprises several villages divided into 7 ethnic groups (Bagyeli, Batanga, Bulu, Lyassa, Mabea, Mvae and Ntumu) that practice community-based land use (settlements, agriculture, and forest access) (CMNP, 2014; UNESCO, 2018; Engolo et al., 2024; Komo Mbarga et al., 2024).

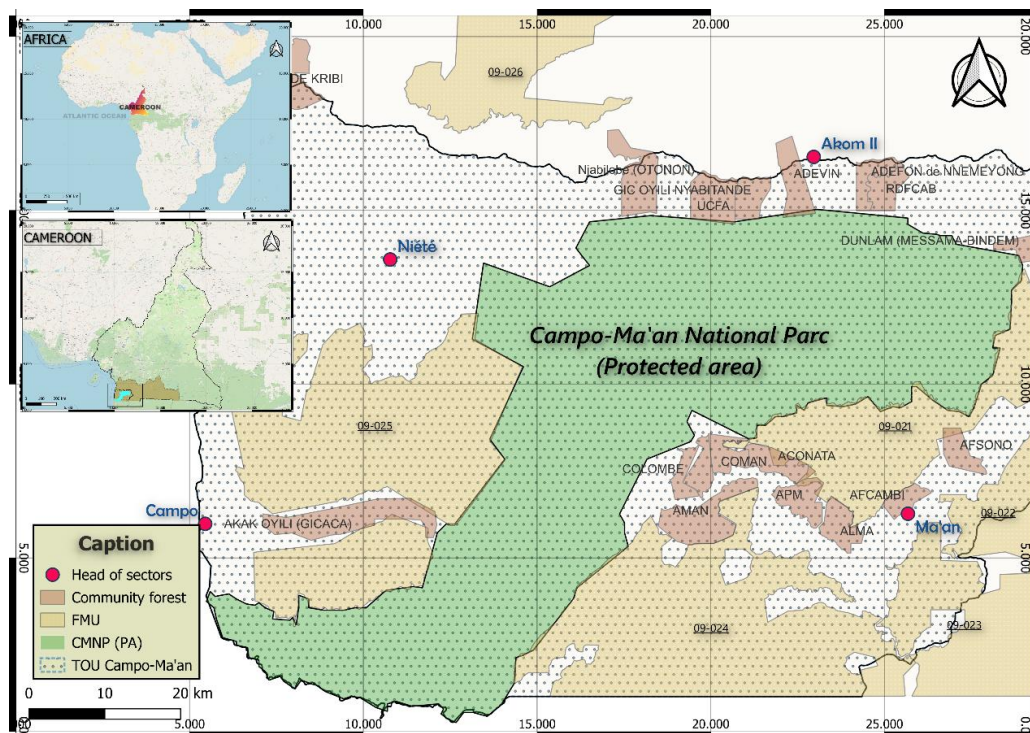


Figure 1: Localization map and description of the Technical Operation Unit Campo-Ma'an

Sampling Design

Fieldwork was conducted across 104 days from August 2023 to February 2025, throughout 5 field trips, covering all 4 climatic seasons (SRS, SDS, GRS, and GDS), with 26 sampling days per season to capture seasonal variation in bat species composition and activity. Twenty fixed sites were established within villages and protected areas, distributed across 4 park stations and buffer zones (Supplementary support [S1](#)). These sites encompass primary forest, secondary forest, farms (cocoa, banana, and rubber plantations), and human habitats (villages, ecolodges, residential backyards, and school grounds) (Figure 2), geographical coordinates of all capture places are found in Supplementary support ([S2](#)).

At each site, multiple capture locations were selected, including forest edges, bridges, roofs, cocoa and banana farms, near-water habitats and watercourses (Ajonina et al., 2010;

Atagana et al., 2021). Sites were visited 3-5 times (mean = 3.65 nights/site) following Grunwald et al. (2025), yielding a total of 80 sampling nights, 73 of which were successful.

Mist nets (5-10 per site; mean = 6, lengths of 18 m, 12 m, 9 m and 6 m, 16-mm mesh; Ecotone, Poland) mounted on ~3 m high poles were placed in flyways, forest gaps, and near water points (Kunz et al., 2011). Nets and traps were opened from 18:00 - 05:00 h and nets were checked every 15 min. Total mist net sampling effort was calculated by multiplying the number of successful sampling nights by the exposure time and the average number of nets opened, resulting in 5,256 net-hours (Falcão et al., 2018). A harp trap (1.8 m × 1.5 m; Austbat, Australia) was placed across narrow forest paths or cave entrances, totaling 876 trap-hours. In addition, a triple-high mist net system (three 12 m × 2.6 m nets stacked to 7.8 m; Ecotone, Poland) was deployed twice at site 3 (near bootcamp 3) before it broke.

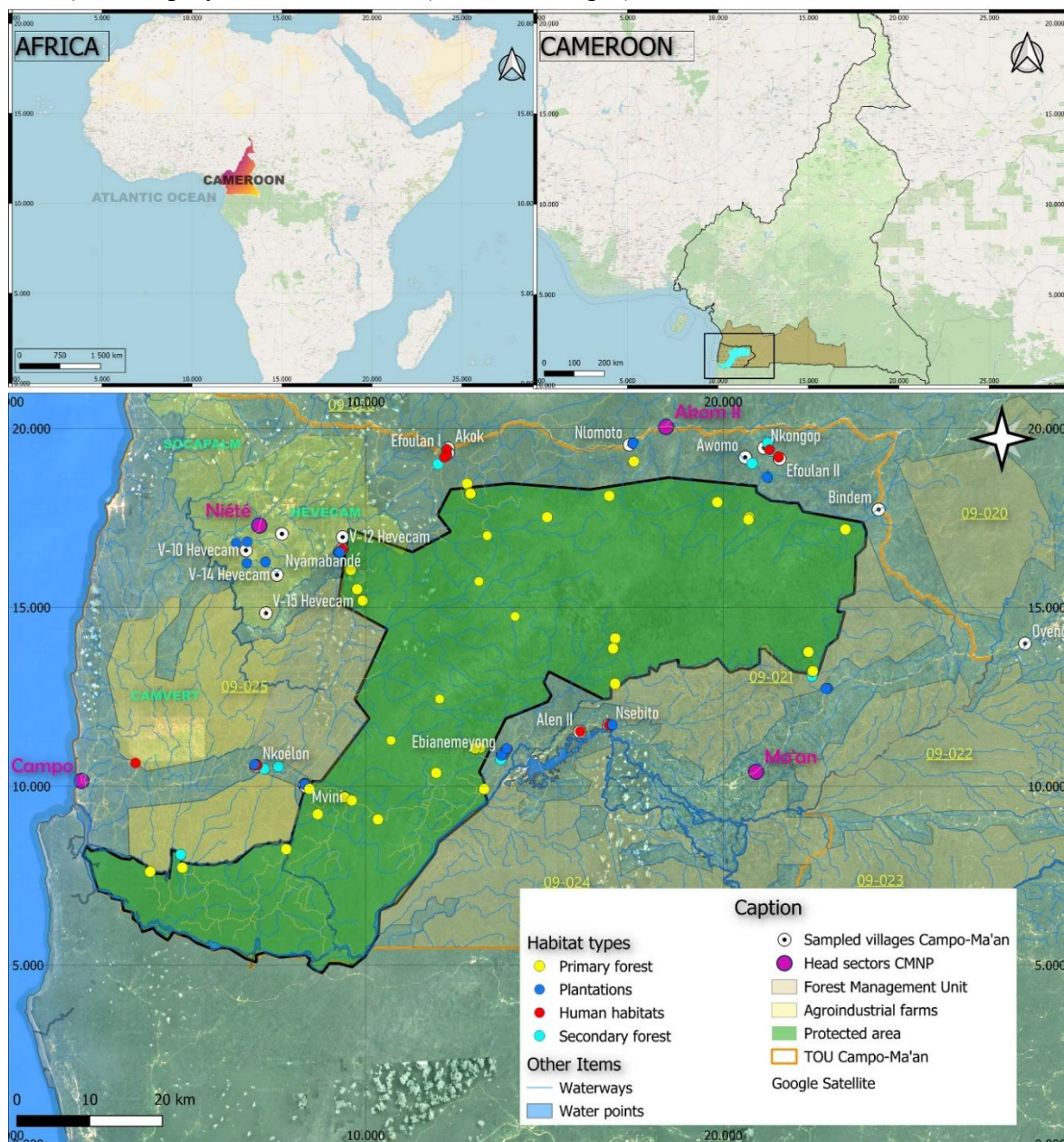


Figure 2: Sampling points on the study site

Acoustic monitoring with active recorder

Active recordings were taken using an Anabat Walkabout (Titley Scientific, Australia) to aid species identification and build a preliminary reference call library. We recorded resting phase calls in hand for high-duty cycle species (Rhinolophidae, Hipposideridae). Nycteridae and Vespertilionidae were recorded in flight within a 2 × 4 m mosquito-net flight tent (Hintze et al., 2021; Grunwald et al., 2025).

Species Identification

Captured bats were identified using regional taxonomic keys (Patterson & Webala, 2012; Happold & Happold, 2013; Monadjem, 2020; Van Cakenberghe & Seamark, 2025). External characters were taken using calipers (± 0.1 mm), including forearm, tibia, body, ear, tail, and tragus length (when present). We measured body mass with a digital scale (± 0.1 g) and recorded sex, age, and reproductive status. For hard-to-identify groups, wing membrane biopsies were taken for identification via DNA sequencing, following established protocols (Sikes & the Animal Care and Use Committee of the American Society of Mammalogists, 2016). After processing and labeled on the field as CPM (Campo Project Meyo) followed by the number of the individual, bats were released near capture sites. Select voucher specimens (prefixed "FM," Franck Meyo) were preserved in 70% ethanol and deposited at the Laboratory of Biology and Physiology of Animal Organisms, University of Douala, Cameroon.

Acoustic data were analyzed using Kaleidoscope Pro (v5.8.1, Wildlife Acoustics). Calls were identified based on peak frequency, characteristic frequency, call duration, and sonotype (Bakwo Fils et al., 2018; Monadjem, Peter John Taylor, et al., 2020), using a preliminary CMNP call library developed from recorded individuals (MacSwiney et al., 2008; Walters et al., 2013). Ambiguous calls were assigned to genus or family or excluded from species-level analyses.

Habitat characterization

To characterize habitat types used by bats, we analyzed species occurrence, abundance, and ecological associations across the 4 habitat types (primary forest, secondary forest, farms, human habitats). Capture data from mist nets and harp traps were compiled to quantify species richness and abundance per habitat (Kunz & Parsons, 2009). Capture locations and associated features, including proximity to fruit trees, watercourses, and anthropogenic structures, were recorded to describe habitat preferences, as these features are known to influence bat foraging and roosting behavior (Lobova et al., 2009; Fahr & Kalko, 2011).

Environmental variables, such as vegetation structure (dense canopy vs. open flyways), disturbance level (high, moderate, or low, assessed qualitatively based on observed anthropogenic impact), and altitude (derived from GPS coordinates), were recorded for each site to contextualize ecological niches (Voigt & Kingston, 2016).

Genetics

DNA Extraction

Genomic DNA was extracted from 168 bat tissue samples using the DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany) and the Wizard SV 96 Genomic DNA Purification System, following manufacturer protocols with modifications for bat tissue (Grunwald et al., 2023).

PCR Amplification and sequencing

The entire mitochondrial cytochrome b (cyt-b) gene was amplified using forward and reverse primers (Bickham et al., 1995, 2004), with thermocycler conditions as employed in Grunwald et al. (2023, 2025) for bat DNA barcoding. PCR products were purified using ExoSAP-IT (Thermo Fisher Scientific). Sequencing was performed on an ABI 3100 Genetic Analyzer (Applied Biosystems) at the Pritzker Laboratory for Molecular Systematics and Evolution (Field Museum of Natural History, Chicago, IL, USA).

Data Analysis

Diversity and habitat-season assemblage patterns

Bat assemblage diversity and abundance were characterized across the 4 habitat types (primary forest, secondary forest, human habitats and farms) and 4 climatic seasons (GRS, GDS, SRS, SDS). Diversity metrics, including Simpson's index (D), Shannon diversity (H'), and Pielou's evenness (J'), were calculated using PAST3 software (Hammer et al., 2001) due to its robustness for small sample sizes (Webala et al., 2019).

Species richness was estimated using the Chao 1 estimator in PAST3 to account for unobserved species. Sample-size-based rarefaction and extrapolation (R/E) curves with 95% confidence intervals for species richness ($q = 0$) were generated using abundance data in R (v4.5.1) with the iNEXT.3D and iNEXT.4steps packages (Chao et al., 2014, 2021; Grunwald et al., 2025). These analyses allowed comparison of diversity and abundance patterns among habitats and seasons.

Environmental factors influencing species distributions

To evaluate the combined effects of habitat type and season on bat assemblage structure, we conducted multivariate analyses. Analysis of Similarities (ANOSIM) and Permutational Multivariate Analysis of Variance (PERMANOVA), with 9,999 permutations, were performed in PAST3 using Bray-Curtis dissimilarity to test for differences in species composition across habitat-season combinations (Clarke, 1993; Anderson, 2017).

Non-metric Multidimensional Scaling (NMDS) in PAST3 was used to visualize assemblage patterns, with stress values indicating ordination fit (Kruskal, 1964; Clarke & Warwick, 2001). Similarity Percentage (SIMPER) analysis in PAST3 identified species contributing most to dissimilarity between habitat-season combinations, quantifying their relative contributions (Clarke, 1993). These analyses collectively assessed how environmental factors, such as habitat type and seasonal climatic variation, shape bat community structure and distribution (Patterson & Webala, 2012; Voigt & Kingston, 2016).

Habitat types used by bats

Capture site characteristics, including proximity to fruit trees, watercourses, and anthropogenic features, were summarized to describe habitat-specific ecological niches, in order to assess bat habitat use (Meyer et al., 2004; Newton, 2007; Kunz & Parsons, 2009). Altitude ranges were extracted from GPS data to assess elevational preferences, which influence bat distributions (McCain, 2006).

These analyses generated a detailed profile of bat habitat use, highlighting the influence of fruit trees, watercourses, and disturbance levels on species distributions in CMNP. Results were

organized into species accounts, arranged phylogenetically by family and alphabetically by genus and species (Teeling et al., 2005; Patterson & Webala, 2012).

DNA Sequence and cyt-b analysis

Cyt-b sequences were assembled and edited using GENEIOUS PRIME v.2024.0.5 (Biomatters Ltd., Auckland, New Zealand). Alignments were generated with MUSCLE (Edgar, 2004) using default settings, following Grunwald et al. (2023, 2025). The cyt-b protein-coding sequences were translated into amino acids to verify codon positions and confirm the absence of premature stop codons, deletions, or insertions.

For species identification, we performed BLASTN searches (Zheng Zhang et al., 2000) against the NCBI nucleotide database (nr/nt) using default parameters (threshold E-value < 0.05; mismatch scores 1, -2). Complete BLAST-N results for all 168 sequenced specimens are provided in Supplementary support (Table S3). Queries consisted of trimmed cyt-b consensus sequences (~1,140 bp) from 168 samples, retaining top hits where alignments covered >95% of query length and nucleotide identity exceeded 96%, a conservative threshold for bat species-level resolution via cyt-b barcoding. This approach confirmed identifications and resolved initial morphological misidentifications and, we downloaded reference sequences and constructed maximum likelihood (ML) trees for these misidentified taxa.

Results

We captured a total of 625 bats, representing 32 species across 20 genera and 6 families (Table 1). The most abundant species were *Hipposideros cf. ruber* (172 individuals; 27.52%), *Megaloglossus woermanni* (124; 19.84%) and *Epomops franqueti* (93; 14.88%). In contrast, 10 species were represented by a single individual: *Casinonycteris campomaanensis*, *Myonycteris angolensis*, *Rhinolophus denti*, *Miniopterus inflatus*, *Kerivoula lanosa*, *Kerivoula phalaena*, *Myotis dieteri*, *Myotis bocagii*, *Neoromicia sp.*, and *Pseudoromicia roseveari*. Noteworthy records include 2 confirmed first country records (*Rhinolophus denti* and *Myotis dieteri*), 3 potential first country records pending genetic confirmation (*R. cf. blasii*, *R. cf. acrotis*, and *Glauconycteris cf. humeralis*), 1 Endangered species (*Ps. roseveari*), and 2 Data Deficient species (*C. campomaanensis* and *M. dieteri*).

Species accounts

For each bat species we provide IUCN Red List status (IUCN, 2025), new locality records, portraits (Figure 3), and relevant taxonomic and ecological information.

Yinpterochiroptera

Family PTEROPODIDAE Gray, 1821

Genus *Casinonycteris* Thomas, 1910

Table 1 : Overview of bats sampled and morphological measurements of each bat species collected in the CMNP:

Weight= mass in grams (g); B=wingspan in millimeters (mm); FA= forearm length; Tib= tibia length; ToL= body length; Tail= tail length; Ear= ear length; Tragus= tragus length; SD= standard deviation; Mean= average value; **=first record in Cameroon.

Family/Species	Count (sex)(Diet)(IUC N Status)	Weight (g)		B (mm)		FA		Tib		ToL		Tail		Ear		Tragus	
		Mean ± SD	Range	Mean ± SD	Rang e	Mean ± SD	Range	Mea n ± SD	Rang e	Mean ± SD	Rang e	Mea n ± SD	Rang e	Mea n ± SD	Rang e	Mea n ± SD	Rang e
Pteropodidae	356																
<i>Casinycteris campomaanensis</i>	1♀ (F) DD	55	-	47	-	70	-	31	-	75	-	-	-	21	-	-	-
<i>Epomops franqueti</i>	93 (68♀♀, 25♂♂) (F) LC	114,6 2	12 -	55,79 ±	27 -	89,49 ±	62 -	35,11 ±	29 -	102,8 2	75 -	-	-	25,12 ±	20 -	-	-
		44,42	218	5,93	71	6,1	110	2,71	41	10,94	130	-	-	2,41	30	-	-
<i>Hypsignatus monstrosus</i>	5♂♂ (F) LC	252,2 5	221 -	74,75 ±	72 -	121,2 5	120 -	50,75 ±	48 -	146,2 5	143 -	-	-	30 ±	28 -	-	-
		27,78	285	2,99	79	0,96	122	2,22	53	3,3	150	-	-	2,16	33	-	-
<i>Megaloglossus woermanni</i>	123 (94♀♀, 29♂♂) (N) LC	18,06 ±	6 -	28,37 ±	24 -	42,64 ±	37 -	18,56 ±	13 -	50,05 ±	40 -	37,5 ±	20 -	14,7 ±	12 -	13	-
		15,85	139	4,06	58	4,62	89	2,37	34	6,41	93	24,75	55	1,75	26	-	-
<i>Myonycteris angolensis</i>	1♀ (F) LC	102	-	51	-	81	-	34	-	90	-	12	-	20	-	-	-
<i>Myonycteris torquata</i>	29 (22♀♀, 7♂♂) (F) LC	35,75 ±	18 -	38,41 ±	33 -	59,79 ±	51 -	23,34 ±	20 -	69,17 ±	61 -	9,91 ±	8 -	15,76 ±	13 -	-	-
		7,03	45	3,25	46	2,61	65	1,56	27	5,46	88	1,12	12	1,68	20	-	-
<i>Rousettus aegyptiacus</i>	87 (42♀♀, 45♂♂) (F) LC	150,2 4	17 -	56,46 ±	44 -	94,82 ±	74 -	43,75 ±	30 -	100,2 2	9 -	17,11 ±	9 -	20,9 ±	17 -	-	-
		40,37	239	5,2	69	7,48	113	4,55	53	17,97	180	2,92	23	1,45	24	-	-

Family/Species	Count (sex)(Diet)(IUC N Status)	Weight (g)		B (mm)		FA		Tib		ToL		Tail		Ear		Tragus	
		Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range
<i>Scotonycteris zenkeri</i>	16 (13♀♀, 3♂♂)	16,93	9	31,19	24	49,06	43	21,88	18	50,13	20			13,93	12		
	(F) NT	±	-	±	-	±	-	±	-	±	-	32	-	±	-	-	-
		4,67	25	3,21	36	2,91	54	7,33	49	10,27	61			1,03	15		
Hipposideridae	197																
<i>Doryrhina cyclops</i>	14 (8♀♀, 6♂♂)	27	8	36,85	34	64,36	49	31,79	19	62,57	41	26,64	21	27,93	16		
	(I) LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		9,05	46	1,91	41	4,76	69	3,93	35	7,84	71	3,39	31	4,48	33		
<i>Hipposideros beatus</i>	11(2♀♀, 9♂♂)	9,09	5	24,64	23	43	40	15,36	14	36,64	35	23,44	16	13,64	12		
	(I) LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		4,72	18	2,01	28	3,13	50	1,75	20	2,06	41	3,88	28	1,36	16		
<i>Hipposideros ruber</i>	172 (117♀♀,	9,54	6	28,59	16	49,94	39	20,18	14	41,84	32	29,76	20	14,55	11		
	55♂♂) (I) LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		2,21	17	2,27	35	2,25	61	1,4	29	3,39	53	3	39	1,43	19		
Rhinolophidae	33																
<i>Rhinolophus alcyone</i>	9 (6♀♀, 3♂♂) (I)	14,78	10	31,56	29	51,78	49	24,11	22	46,22	43	23,22	20	21,33	20		
	LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		3,15	20	1,74	34	1,56	54	0,93	25	2,28	49	2,22	27	1	22		
<i>Rhinolophus cf. acrotis</i>	5 (2♀♀, 3♂♂) (I)	14,4	9	35,2	26	51,2	50	23,4	20	43,6	42	24,4	21	21,8	14		
	LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		3,51	18	12,93	58	1,3	53	2,19	26	0,89	44	2,97	29	4,49	25		
<i>Rhinolophus cf. blasii</i>	5 (2♀♀, 3♂♂) (I)	13,4	9	27,8	26	44,8	41	20,4	18	42	35	21,8	19	17,6	15		
	LC	±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		4,72	20	1,92	31	4,28	52	3,29	26	6,78	52	3,63	28	1,95	20		
<i>Rhinolophus denti</i>	1♂ (I) LC	10	10	27	-	49	-	20	-	38	-	18	-	20	-	-	-
<i>Rhinolophus landeri</i>	13 (5♀♀, 8♂♂) (I) LC	8,31	7	27,38	26	43,77	42	20,08	13	38	32	24,46	21	16,92	13		
		±	-	±	-	±	-	±	-	±	-	±	-	±	-	-	-
		1,25	10	1,19	29	0,83	45	3,8	29	3,74	44	2,07	28	1,98	22		

Family/Species	Count (sex)(Diet)(IUC N Status)	Weight (g)		B (mm)		FA		Tib		ToL		Tail		Ear		Tragus	
		Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range	Mean ± SD	Range
<i>**Myotis dieteri</i>	1♂ (I) DD	5	5	27	-	38	-	19	-	39	-	41	-	19	-	7	-
<i>Neoromicia</i> sp.	1♂ (I) NA	2	2	23	-	35	-	15	-	30	-	36	-	10	-	5	-
<i>Pipistrellus nanulus</i>	2♂♂ (I) LC	12 ±	4 -	21 ±	18 -	30,5 ±	27 -	13 ±	12 -	38 ±	34 -	27 ±	24 -	11,5 ±	10 -	6 ±	-
<i>Pipistrellus</i> sp.	2♂♂ (I) NA	11,31 3 ±	20 3 -	4,24 20,5 ±	24 20 -	4,95 30,5 ±	34 30 -	1,41 13,5 ±	14 13 -	5,66 38 ±	42 38 -	4,24 30,5 ±	30 30 -	2,12 10,5 ±	13 10 -	0 4,5 ±	- 4 -
<i>Pseudoromicia roseveari</i>	1♀ (I) EN	4	4	24	-	37	-	15	15	40	-	32	-	12	-	6	-
<i>Scotophilus nux</i>	8 (4♀♀, 4♂♂) (I) LC	29,75 ±	25 -	35,75 ±	34 -	57 ±	54 -	22,88 ±	20 -	63,88 ±	60 -	47,88 ±	41 -	14,88 ±	13 -	9 ±	7 -
<i>Myotis bocagii</i>	1♂ (I) LC	3,92	36	1,67	38	1,93	60	1,81	26	3,68	72	4,19	54	1,46	17	1,07	10

Casinycteris campomaanensis Hassanin, 2014
Campo Ma'an Fruit Bat (Figure 3A)

IUCN Red List status: Data Deficient

New locality records: A single adult female of *Casinycteris campomaanensis* was captured during the third field trip, in the SRS at Site 8, located in the northern sector of the park along a watercourse in primary forest (2.733345, 10.308223; 188 m). The site featured dense canopy cover and very low anthropogenic disturbance. No additional individuals were noted across the 19 other sites, seasons, or habitat types.

Notes: The individual was captured on 29 April 2024 at approximately 05:00 h under light rainfall. This capture represents only the second documented locality for this species near its type area, reinforcing the species' rarity and restricted distribution.

Genus *Epomops* Gray, 1866

Epomops franqueti (Tomes, 1860)
Franquet's Epauletted Fruit Bat (Figure 3B)

IUCN Red List status: Least Concern

New locality records: A total of 94 *Epomops franqueti*, including 70♀♀, and 24♂♂ were captured across all 20 sampling sites and throughout all 4 seasons (GRS: 30; GDS: 28; SRS: 17; SDS: 19). The species was recorded in all habitat types, including primary forest (10 individuals), secondary forest (11), human habitats (31), and farms (42).

Captures occurred in a wide variety of settings, included ecolodge courtyards (Nkoelone village), hospital and school grounds (Efulan I village), residential backyards and courtyards, agroforestry plots near fruit trees (*Annona muricata*, *Carica papaya*, *Cola acuminata*, *Dacryodes edulis*, *Garcinia kola*, *Mangifera indica*, *Psidium guajava*), banana, cocoa, and rubber plantations (with watercourses), palm groves, Chinese bamboo stands, rocky forest patches, bridges, and along several watercourses (e.g., Dounba'andou, Grand Medibane, Bitandé, Njo'o).

Notes: Individuals were captured under a wide range of weather conditions, including clear, lightly clouded, and overcast skies, with and without rainfall, and occasionally under noticeable moonlight.

Genus *Hypsignathus* H. Allen, 1861

Hypsignathus monstrosus H. Allen, 1861
Hammer-headed Fruit Bat (Figure 3C)

IUCN Red List status: Least Concern

New locality records: A total of 5 adult females *Hypsignathus monstrosus* were captured during 2 field trips in the GRS (3) and SDS (2). Individuals were recorded in 3 habitat types: primary forest (3), secondary forest (1), and human habitats (1).

Capture locations included Chinese bamboo stands (2.368426, 10.1096; 72 m and 2.368107, 10.10958; 71 m), CAMVERT fence entry (2.399981, 9.894684; 79 m), a swamp (2.700214, 10.65178; 575 m), and primary forest interior (2.413101, 10.351155; 399 m).

Notes: All captures occurred under calm conditions (no strong wind), without rainfall, and in the absence of moonlight. Three individuals were netted around 19:00 h shortly after sunset, and 2 at approximately 05:00 h just before net closure, suggesting bimodal activity peaks (early evening and very late night/pre-dawn).

Genus *Megaloglossus* Pagenstecher, 1885

Megaloglossus woermanni Pagenstecher, 1885

Eastern Woermann's Fruit Bat (Figure 3D)

IUCN Red List status: Least Concern

New locality records: A total of 123 *Megaloglossus woermanni*, including 94♀♀, and 29♂♂ were captured across 14 of the 20 sampling sites during all 5 field trips and throughout all 4 seasons (GRS: 14; GDS: 54; SRS: 13; SDS: 42). The species was recorded in all 4 habitat types with a single individual in primary forest, 3 in secondary forest, 46 in human habitats, and 73 in farms (indicating a preference for disturbed environments).

Capture settings included residential backyards and courtyards, hospital grounds, agroforestry plots near fruit trees (*Annona muricata*, *Carica papaya*, *Dacryodes edulis*, *Mangifera indica*, *Psidium guajava*), cassava farms, banana, cocoa, and rubber plantations (with watercourses), palm groves, watercourses, water points, and forest edges.

Notes: Individuals were captured under a wide range of weather conditions, including evenings with noticeable moonlight, and during both rainy and dry conditions.

Genus *Myonycteris* Matschie, 1899

Myonycteris angolensis (Bocage, 1898)

Angolan Soft-furred Fruit Bat (Figure 3E)

IUCN Red List status: Least Concern

New locality records: A single lactating adult female *Myonycteris angolensis* was captured during the 4th field trip at Site 11 (near FMU 09-024) in Nko'o-Ngop village, within a human-modified habitat behind classrooms at a public school (2.777339, 10.689064; 634 m), during the SDS.

Notes: The individual was captured on 19 July 2024 at approximately 05:00 h in a 12 m mist net under light rainfall.

Myonycteris torquata (Dobson, 1878)

Little Collared Fruit Bat (Figure 3F)

IUCN Red List status: Least Concern

New locality records: A total of 29 *Myonycteris torquata* (22♀♀, 7♂♂) were captured across 9 of the 20 sampling sites during all 5 field trips and throughout all 4 seasons (GRS: 11; GDS: 6; SRS: 10; SDS: 2). The species was recorded in all 4 habitat types with 14 individuals in primary forest, 3 in secondary forest, 4 in human habitats, and 8 in farms.

Capture locations included agroforestry plots near fruit trees (*Annona muricata*, *Carica papaya*, *Cola acuminata*, *Dacryodes edulis*, *Garcinia kola*, *Mangifera indica*, *Psidium guajava*), hospital backyards, residential courtyards, cocoa plantations, forest interiors, and along watercourses, including Grand Medibane (2.600243, 10.175231; 105 m) and Njo'o (2.51331, 10.731341; 537 m).

Notes: No individuals were captured between 22:00 h and midnight, suggesting limited late-night activity.

Genus *Rousettus* Gray, 1821

Rousettus aegyptiacus (É. Geoffroy Saint-Hilaire, 1810)

Egyptian Rousette (Figure 3G)

IUCN Red List status: Least Concern

New locality records: A total of 87 *Rousettus aegyptiacus* (42♀♀, 45♂♂) were captured across 14 of the 20 sampling sites during 4 field trips (absent during the second field trip) and throughout all 4 seasons (GRS: 7; GDS: 15; SRS: 26; SDS: 39). The species was recorded in all 4 habitat types with 12 individuals in primary forest, 11 in secondary forest, 48 in human habitats, and 16 in farms.

Capture settings included ecolodge backyards, school grounds, residential backyards and courtyards, bridges, Chinese bamboo stands, palm groves, cocoa and banana plantations, and forest galleries along watercourses (Otong Mekok: 2.541313, 10.484906; 464 m; Bitandé, Ongat, Manebingang).

Notes: Individuals were captured under a wide range of weather conditions, including evenings with noticeable moonlight and both rainy and dry conditions. Captures occurred during every hourly interval after sunset, indicating continuous nocturnal activity.

Genus *Scotonycteris* Matschie, 1894

Scotonycteris zenkeri Matschie, 1894

Zenker's Fruit Bat (Figure 3H)

IUCN Red List status: Near Threatened

New locality records: A total of 16 *Scotonycteris zenkeri* (13♀♀, 3♂♂) were captured across approximately 10 of the 20 sampling sites during all 5 field trips and throughout all 4 seasons (GRS: 5; GDS: 5; SRS: 4; SDS: 2). The species was recorded in all 4 habitat types with 9 individuals in primary forest, 3 in secondary forest, 1 lactating female in human habitat (backyard of chieftaincy, Oveng village: 2.413555, 10.350639; 395 m), and 3 in farms (including 1 female with dependent young in a cocoa plantation near Nyamabandé: 2.66007, 10.145389; 62 m). Capture locations included forest galleries along Otong Mekok (2.541429,

10.485057; 467 m), Biwomé mangrove watercourse (2.553669, 10.4873; 506 m), rocky forest, palm groves, cocoa plantations, residential backyards and courtyards, and various watercourses.

Notes: All captures occurred under calm and dry conditions with no moonlight.

Family HIPPOSIDERIDAE Lydekker, 1891

Genus *Doryrhina* Peters, 1871

Doryrhina cyclops (Temminck, 1853)

Cyclops Roundleaf Bat (Figure 3I)

IUCN Red List status: Least Concern

New locality records: A total of 14 *Doryrhina cyclops*, including 8♀♀, and 6♂♂ were captured across 7 of the 20 sampling sites, during all 5 field trips and throughout all 4 seasons (GRS: 5; GDS: 5; SRS: 1; SDS: 3). The species was recorded in all 4 habitat types with 4 individuals in primary forest, 5 in secondary forest, 3 in human habitats, and 2 in farms, suggesting a generalist distribution. Capture locations included Chinese bamboo stands, residential backyards and courtyards, clearings, cocoa plantations, watercourses, rocky forest patches, forest under *Artocarpus altilis* (2.358411, 10.153385; 107 m), Grand Medibane (2.600776, 10.175039; 120 m), Manebingang (2.330306, 10.19412; 187 m), and forest gallery along Otong Mekok (2.541229, 10.484688; 455 m).

Notes: Captures showed no clear peak activity period and occurred predominantly under calm and dry conditions with no moonlight.

Genus *Hipposideros* Gray, 1831

Hipposideros beatus K. Andersen, 1906

Benito Roundleaf Bat (Figure 3J)

IUCN Red List status: Least Concern

New locality records: A total of 11 *Hipposideros beatus*, including 2♀♀, and 9♂♂ were captured across 7 of the 20 sampling sites during 4 field trips (absent during the second trip) and throughout all 4 seasons (GRS: 3; GDS: 5; SRS: 2; SDS: 1). The species was recorded in 2 habitat types only: primary forest (5 individuals) and farms (5 individuals), with no captures in secondary forest or human habitats. Capture locations included watercourses at Grand Medibane (2.600905, 10.174883; 128 m), clearings, cocoa plantations, palm groves (2.647745, 10.055261; 54 m), and rubber plantations with watercourses in forest pockets (2.646676, 10.032277; 36 m).

Notes: Most individuals (6) were captured in the harp trap and none after 21:30 h, suggesting limited late-night activity. Weather conditions appeared to have no strong influence.

Hipposideros cf. ruber (Noack, 1893)

Noack's Roundleaf Bat (Figure 3K)

IUCN Red List status: Least Concern

New locality records: A total of 172 *Hipposideros cf. ruber*, including 117♀♀, 55♂♂ were captured across 19 of the 20 sampling sites (the site 4 excluded), during all 5 field trips and throughout all 4 seasons (GRS: 37; GDS: 71; SRS: 16; SDS: 48). The species was recorded in all 4 habitat types with 58 individuals in primary forest, 62 in secondary forest, 15 in human habitats, and 37 in farms. Capture locations were highly diverse and included Picarthian cave (2.395564, 10.071189; 138 m), Ongat watercourse (2.358388, 10.153003; 91 m), bridges, clearings, rubber plantations with watercourses, Chinese bamboo (triple-high net capture at 2.367991, 10.109575; 70 m), uninhabited ecolodge, residential backyards in Efulan I (2.786832, 10.278974; 79 m), northern primary forest watercourse (2.733096, 10.308123; 202 m), farms in Nlomoto (2.793706, 10.511042; 413 m), multiple caves, Awomo watercourse (2.769491, 10.656395; 641 m), Ntebe Zok watercourse, swamps, palm groves, house roofs in Minkan Mengalé (2.438856, 10.444126; 394 m), banana plantations, Njo'o watercourse (2.51331, 10.731341; 537 m), and cocoa plantations.

Notes: No specific activity peak hour or strong weather preference was observed. Acoustic data (n = 126 individuals) showed high variability in peak frequency (SD = ±41.25 kHz), suggesting intraspecific variation potentially linked to sex, age, or cryptic lineage differences within the sampled population.

Family RHINOLOPHIDAE Gray, 1825

Genus *Rhinolophus* Lacépède, 1799

Rhinolophus cf. acrotis Heuglin, 1861

Eritrean Horseshoe Bat (Figure 3N)

IUCN Red List status: Least Concern

Previous distribution and range extension: *Rhinolophus cf. acrotis* is traditionally associated with the Saharo-Sindian and Ethiopian arid zones, extending from the Arabian Peninsula through the Horn of Africa to Egypt and Sudan (Happold & Happold, 2013). It is typically found in desert, semi-desert, and montane shrubland habitats (Happold & Happold, 2013). There are no historical or recent records of this species in the Guineo-Congolian rainforest biome or within the Central African region in the literature, including the ACR (2025) and GBIF (2026). Our captures in the Campo-Ma'an landscape could represent a significant southwestward range extension and, pending further genetic confirmation, the first documented record of the species for Cameroon.

New locality records: A total of 5 *Rhinolophus cf. acrotis*, including 2♀♀, and 3♂♂ were captured during 2 field trips across 3 sampling sites during the SDS (3) and GDS (2). The species was recorded in human habitats (2), cocoa farms (1), and secondary forest (2). Specific locations included residential backyards in Oveng (2.410806, 10.348323; 405 m), human habitat and cocoa farms in Ebianemeyong (2.417399, 10.354154; 403 m), and secondary forest near a watercourse in Minkan Mengalé (2.506923, 10.730359; 515 m).

Notes: All captures occurred under slightly cloudy skies at mid-elevation (403-515 m), with no individuals recorded after 20:00 h. We initially misidentified individuals as *R. clivosus* because of their morphological similarity, but as this species isn't documented for the region, the most likely identification is *R. cf. acrotis* (Dool et al., 2016; Demos et al., 2019; Uvizl et al., 2024). Morphologically, the species is distinguished by a large, rounded sella and a high-set, pointed lancet (Happold & Happold, 2013). While typically considered a cave-roosting species in arid landscapes, its occurrence in human habitats and cocoa farms in Cameroon suggests a high degree of ecological flexibility and potential use of anthropogenic structures or rocky outcrops within the forest-farm mosaic.

Rhinolophus alcyone Temminck, 1853
Halcyon Horseshoe Bat (Figure 3L)

IUCN Red List status: Least Concern

New locality records: A total of 9 *Rhinolophus alcyone*, including 6♀♀, and 3♂♂ were captured across approximately 7 of the 20 sampling sites during 3 field trips and throughout 3 seasons (GRS: 1; GDS: 6; SDS: 2; absent in SRS). The species was recorded in all 4 habitat types with 4 individuals in primary forest, 3 in secondary forest, 1 in human habitat, and 1 in farms. Capture locations included a clearing in secondary forest (2.355413, 10.15991; 138 m), Awomo watercourse in secondary forest near Nko'o-Ngop (2.769491, 10.656395; 641 m), cocoa plantation in Ebianemeyong (2.417732, 10.353455; 407 m), Petit Medibane watercourse in primary forest (2.613903, 10.168109; 229 m), residential backyard in Nsebito (2.44694, 10.480947; 408 m), Njo'o watercourse in primary forest (2.497915, 10.487032; 410 m), and a water point in FMU 09-025 near Minkan Mengalé (2.506923, 10.730359; 515 m).

Notes: All specimens were captured under calm, dry conditions with no moonlight, and none after 21:30 h. Acoustic data (resting phase calls) showed characteristic constant-frequency (CF) calls typical of the genus ($F_c \approx 71$ kHz), consistent with published records for Central African populations (Monadjem et al., 2020).

Rhinolophus cf. blasii Peters, 1866
Blasius's Horseshoe Bat (Figure 3M)

IUCN Red List status: Least Concern (LC).

Previous distribution and range extension: *Rhinolophus cf. blasii* exhibits a remarkably disjunct distribution across the Palearctic and Afrotropic regions, with known populations in the Mediterranean, East Africa (Ethiopia to Kenya), and Southern Africa (Malawi to South Africa) (Monadjem et al., 2020). In West Africa, records are sparse and limited to highland or savanna areas in Guinea, Sierra Leone, and Nigeria (Happold & Happold, 2013; Monadjem et al., 2020). There are currently no documented records for this species in the humid coastal forests of Cameroon in the literature, including the African Chiroptera Report (Van Cakenberghe & Seamark, 2025) or GBIF (2026). The current captures could represent a significant range extension into the Lower Guinea rainforest block and, pending genetic verification, the first documented record of the species for Cameroon.

New locality records: A total of 5 *Rhinolophus cf. blasii*, including 2♀♀, and 3♂♂ were captured during 2 field trips across 4 of the 20 sampling sites during the SRS (2) and SDS (3). Individuals were recorded in primary forest (1), secondary forest (2), and farms (2). Specific locations included a watercourse in primary forest (North Park: 2.7444, 10.30446; 162 m), cocoa farms in Nlomoto (2.795146, 10.50926; 403 m), secondary forest near Awomo in Nko'o-Ngop (2.752952, 10.67675; 629 m), and cocoa farms in Oveng (2.409485, 10.346539; 404 m). **Notes:** Captures occurred under a wide range of weather conditions across a mid-elevation gradient (162-667 m). Morphologically, *R. blasii* is distinguished by its wedge-shaped sella and a connecting process that rises to a point, forming a continuous curve with the lancet (Monadjem et al., 2020). While it is typically regarded as a cave-roosting species found in more open landscapes, its presence in both primary forest and cocoa farms suggests an ability to exploit forest-edge ecotones and agro-ecosystems.

Rhinolophus denti Thomas, 1904
Dent's Horseshoe Bat (Figure 3O)

IUCN Red List status: Least Concern (LC).

Previous distribution and range extension: *Rhinolophus denti* has a notably disjunct distribution. It is primarily known from the arid regions of Southern Africa (Namibia, Botswana, South Africa) and isolated parts of West Africa (Guinea, Ghana, Nigeria) (Happold & Happold, 2013; Monadjem et al., 2020). There are currently no georeferenced records for this species within the humid rainforests of the Congo Basin or the coastal zones of Cameroon in the African Chiroptera Report (Van Cakenberghe & Seamark, 2025) or GBIF (2026). This record from Mvini represents the first genetically confirmed occurrence of *R. denti* in Cameroon (though *R. cf. denti* was previously recorded morphologically at one locality) and a significant habitat extension into the humid tropical forest biome.

New locality records: A single juvenile male of *Rhinolophus denti* was captured during the first field trip at bootcamp site 3 in human habitat, specifically under an ecolodge roof in Mvini (2.372825, 10.104516; 118 m), during the Great Rainy Season (GRS). The individual was initially misidentified as *Rhinolophus landeri* due to its small size and similar noseleaf morphology, but cyt-b analyses confirmed its identity as *R. denti*.

Notes: The capture occurred on 27 August 2023 at midnight under dry conditions. Its discovery in an ecolodge roof suggests that *R. denti* may exhibit high behavioral plasticity, utilizing anthropogenic structures for roosting even within a primary forest matrix. Morphologically, *R. denti* is distinguished from *R. landeri* by its smaller size and the shape of the lancet and sella (Monadjem et al., 2020). While typically considered 1 of the 28 species often underrepresented in standard forest protected area surveys (Montauban et al., 2025), its presence here underscores the importance of sampling anthropogenic "micro-habitats" within national parks. Acoustic data (resting phase) from this juvenile male showed a peak frequency of 71 kHz; adult call parameters may differ.

Rhinolophus landeri Martin, 1838
Lander's Horseshoe Bat (Figure 3P)

IUCN Red List status: Least Concern

New locality records: A total of 13 *Rhinolophus landeri*, including 5♀♀, 8♂♂, (including 1 subadult and 5 juveniles) were captured across 7 of the 20 sampling sites during 4 field trips and throughout 3 seasons (GRS: 3; SRS: 1; GDS: 9). Individuals were recorded in all 4 habitat types with 4 in primary forest, 6 in secondary forest, 1 in human habitat, and 2 in farms. Capture locations were diverse and included secondary forest near a bridge (West Park: 2.358641, 10.153184; 96 m), uninhabited ecolodge on Dipikar Island (2.28617, 9.950391; 33 m), primary forest watercourse (North side: 2.733096, 10.308123; 202 m), Grand Medibane watercourse (2.600776, 10.175039; 120 m), residential backyard in Nsebito (2.44694, 10.480947; 408 m), Njo'o river border in primary forest (2.51331, 10.731341; 537 m), secondary forest water point in Minkan Mengalé (2.512477, 10.72988; 512 m), and cocoa farms in Minkan Mengalé (2.506923, 10.730359; 515 m).

Notes: Captures occurred under varied weather conditions (no rain, light rain, heavy rain, and with moonlight) across a wide altitudinal range (33-571 m), indicating distribution from lowland to mid-elevation habitats. Acoustic data (resting phase calls) showed characteristic frequency (F_c) \approx 101 kHz, consistent with published records for Central African populations (Monadjem et al., 2020).

Yangochiroptera

Family MINIOPTERIDAE Dobson, 1875

Genus *Miniopterus* Bonaparte, 1837

Miniopterus inflatus Thomas, 1903

Greater Long-fingered Bat (Figure 3Q)

IUCN Red List status: Least Concern (LC).

New locality records: A single male of *Miniopterus inflatus* was captured during the first field trip near bootcamp site 2 in a 12 m mist net along the Ongat watercourse in primary forest on the west sector of the park (2.357889, 10.152744; 102 m), during the GRS. No additional individuals were recorded across any other sites, seasons, or habitat types.

Notes: The capture occurred on 16 August 2023 under light rain at low elevation. *Miniopterus inflatus* is typically a cave-dwelling species, but it is known to forage extensively in primary and secondary lowland forests (Happold & Happold, 2013).

Taxonomic Note: The genus *Miniopterus* is characterized by extreme morphological conservatism, making species identification based on external features notoriously difficult (Happold & Happold, 2013). While the individual showed genetic proximity to the *M. fraterculus* complex in initial cyt-b analyses, its morphological characteristics (particularly the forearm length) align it with the *M. inflatus* group present in the Lower Guinea rainforest. *M. inflatus* is widely distributed across Sub-Saharan Africa, but recent molecular studies have identified significant cryptic diversity within this taxon, particularly in Central African populations (Monadjem et al., 2020). Although initial genetic results suggested an affinity with the smaller *M. fraterculus*, we assign this specimen to *M. inflatus* based on FA (45 mm) and

craniodental features that exceed the typical range of the *M. fraterculus* complex (Monadjem et al., 2020a). This highlights the ongoing systematic challenges in distinguishing *M. inflatus* from its smaller congeners in the absence of multi-locus nuclear data (Demos et al., 2020, 2023).

Family NYCTERIDAE Van der Hoeven, 1855

Genus *Nycteris* E. Geoffroy and G. Cuvier, 1795

Nycteris arge O. Thomas, 1903
Bates's Slit-faced Bat (Figure 3R)

IUCN Red List status: Least Concern

New locality records: Two males of *Nycteris arge* were captured at 2 of the 20 sampling sites in different seasons (SRS: 1; GDS: 1). Both individuals were recorded in primary forest along watercourses: North sector of the park (2.744346, 10.304616; 165 m) and Njo'o river in Minkan Mengalé (2.51331, 10.731341; 537 m).

Notes: Captures occurred under short rain and great dry conditions and were captured in mid-elevation (165-537 m) riverine habitats.

Nycteris grandis (Peters, 1865)
Large Slit-faced Bat (Figure 3S)

IUCN Red List status: Least Concern

New locality records: A total of 6 *Nycteris grandis*, including 2♀♀, and 4♂♂ were captured during 3 field trips across 3 of the 20 sampling sites and throughout 3 seasons (GRS: 2; SRS: 2; GDS: 2). Individuals were recorded in 3 habitat types: primary forest (2), human habitat (2), and secondary forest (2). Capture locations included primary forest near Chinese bamboo in west sector of the park (2.367991, 10.109575; 70 m), human habitat near a nozzle in Efoulan I (2.776949, 10.275927; 80 m), and secondary forest near a water point in Minkan Mengalé (2.512467, 10.730073; 502 m and 2.507009, 10.730305; 519 m).

Notes: Captures occurred in dry conditions, across a wide altitudinal range (70-519 m).

Nycteris hispida (von Schreber, 1774)
Hairy Slit-faced Bat (Figure 3T)

IUCN Red List status: Least Concern

New locality records: A single adult male of *Nycteris hispida* was captured during the first field trip at bootcamp site 3 in a 12 m mist net in secondary forest near a watercourse close to Mvini (2.373768, 10.103935; 96 m) during the GRS.

Notes: The capture occurred under dry conditions at low altitude.

Family VESPERTILIONIDAE Gray, 1821

Genus *Afronycteris* Monadjem, Patterson and Demos, 2020

Afronycteris nanus (Peters, 1851)

Banana Serotine (Figure 3U)

IUCN Red List status: Least Concern

New locality records: A total of 3 *Afronycteris nanus*, including 1 female, and 2♂♂ were captured during 3 field trips across 3 of the 20 sampling sites and throughout 3 seasons (GRS: 1; SDS: 1; GDS: 1). Individuals were recorded in 3 habitat types: primary forest (1), human habitat (1), and farms (1). Capture locations included primary forest along Manebingang watercourse (CMNP west sector: 2.330329, 10.194131; 171 m), residential backyards in Oveng (2.413555, 10.350639; 395 m), and banana farms in Minkan Mengalé (2.492157, 10.749797; 558 m).

Notes: Captures occurred under clear or lightly cloudy sky, and across a wide altitudinal range (171-558 m), with apparent association with banana-rich areas.

Genus *Glauconycteris* Dobson, 1875

Glauconycteris alboguttata J. A. Allen, 1917

Striped Butterfly Bat (Figure 3V)

IUCN Red List status: Least Concern

New locality records: A total of 2 female of *Glauconycteris alboguttata* were captured during the first field trip across 2 of the 20 sampling sites in the GRS. Individuals were recorded in 2 habitat types: primary forest (1) and farms (1). Capture locations included primary forest along Ongat watercourse (CMNP west sector: 2.357889, 10.152744; 102 m) and a rubber plantation with watercourse in a forest pocket at HEVECAM (2.671364, 10.019063; 29 m).

Notes: Both captures occurred under light rain conditions at low altitude (29-102 m).

Genus *Glauconycteris* Dobson, 1875

Glauconycteris cf. *humeralis* J. A. Allen, 1917

Spotted Butterfly Bat (Figure 3W)

IUCN Red List status: Data Deficient

Previous distribution and range extension: *Glauconycteris* cf. *humeralis* is 1 of the rarest members of its genus, with a distribution historically limited to the Democratic Republic of the Congo (DRC), specifically the type locality in Medje, and isolated records in Uganda and western Kenya (Happold & Happold, 2013; Monadjem et al., 2020). Recent literature, including the African Chiroptera Report (Van Cakenberghe & Seamark, 2025) and Montauban et al. (2025), shows a total lack of georeferenced records for the Lower Guinea forest block. These captures in Campo-Ma'an National Park represent a significant western range expansion and,

pending multi-locus genetic confirmation, constitute a potential first country record for Cameroon.

New locality records: A total of 6 *Glauconycteris* cf. *humeralis* (4♀♀, 2♂♂) were captured during 4 field trips across 5 sampling sites throughout all 4 seasons (GRS: 1; SRS: 2; SDS: 1; GDS: 2). Individuals were recorded across a spectrum of environments: primary forest (2), secondary forest (2), human habitat (1), and farms (1). Specific locations include primary forest near Chinese bamboo (2.368426, 10.1096; 72 m), secondary forest near a watercourse in Efoulan I (2.778952, 10.279072; 71 m), residential courtyards in Oveng (2.410912, 10.348055; 412 m), secondary forest in Oveng village (2.41302, 10.351191; 396 m), primary forest along Petit Medibane watercourse (2.614448, 10.168479; 229 m), and banana farms in Minkan Mengalé (2.492065, 10.750205; 561 m).

Notes: Captures occurred under dry conditions across a wide altitudinal range (71-561 m), suggesting high ecological versatility. *Glauconycteris* cf. *humeralis* is characterized by distinctive "butterfly" wing patterns and conspicuous white spots on the shoulders (humeralis), which distinguish it from the more common *G. beatrix* (Monadjem et al., 2020). While typically considered a forest specialist, our records in residential courtyards and banana farms align with recent suggestions that some *Glauconycteris* species may utilize mosaic landscapes and forest edges (Montauban et al., 2025).

Taxonomic Note: The taxonomy of *G. cf. humeralis* remains highly uncertain and is currently the subject of ongoing systematic revision. Molecular analyses by Hassanin et al. (2018) have demonstrated significant genetic divergence within the "dark-winged" *Glauconycteris* group, suggesting that many Central African records may represent a complex of cryptic species rather than a single taxon. Furthermore, Tanshi et al. (2019) highlighted the difficulty in using pelage spots alone for diagnosis, as these characters can be variable or overlap with *G. beatrix* in certain regions. Given that our specimens represent a significant range extension into the Lower Guinea block, far from the type locality in the DRC, we apply the "cf." qualifier pending a comprehensive multi-locus comparison with East and Central African voucher specimens to confirm their specific affinities.

Genus *Kerivoula* Gray, 1842

Kerivoula lanosa (A. Smith, 1847)

Lesser Woolly Bat (Figure 3X)

IUCN Red List status: Least Concern

New locality records: A single female of *Kerivoula lanosa* was captured during the third field trip near bootcamp site 7 in a 12 m mist net in human habitat, in the backyard of a house in Efoulan I village (2.786832, 10.278974; 79 m), the capture occurred during the SRS.

Notes: The capture occurred at 05:00 h under calm and dry conditions with no moonlight and at low altitude.

Kerivoula phalaena Thomas, 1912

Spurrell's Woolly Bat (Figure 3Y)

IUCN Red List status: Least Concern

New locality records: A single adult male of *Kerivoula phalaena* was captured during the fifth field trip at bootcamp site 20 in a 12 m mist net in primary forest bordering the Njo'o river (2.51331, 10.731341; 537 m) during the GDS.

Notes: The capture occurred under calm and dry conditions with no moonlight at mid-elevation altitude.

Genus *Myotis* Kaup, 1829

Myotis dieteri M. Happold, 2005

Kock's Myotis (Figure 3Z)

IUCN Red List status: Data Deficient (DD). This species remains listed as Data Deficient because it is known from only a handful of specimens, and almost no information exists on its population size or ecological requirements (Happold, 2019).

Previous distribution and range extension: Until this study, *Myotis dieteri* was considered a restricted-range endemic known exclusively from its type locality at the Grotte du Viaduc, Loudima, in the southern Republic of the Congo (Happold & Happold, 2013). While its presence in the Lower Guinea rainforest block had been suspected, no verified records had been published for Cameroon or neighboring Gabon (Monadjem et al., 2020). Global databases, including GBIF (2025) and the African Chiroptera Report (Van Cakenberghe & Seamark, 2025), contain no prior georeferenced records for Cameroon. This record from Campo-Ma'an National Park represents a significant northern range extension of approximately 750 km and constitutes the first documented occurrence of the species for Cameroon. Crucially, recent spatial analyses of African bat conservation identify *M. dieteri* as 1 of 28 bat species globally that had never been recorded within a protected area (Montauban et al., 2025). Our record from Campo-Ma'an National Park therefore provides the first evidence of this species occurring within a formally protected landscape, elevating the conservation profile of the park as the only known refuge for a species previously thought to exist only in unprotected, potentially threatened habitats.

New locality records: A single adult male was captured during the fifth field trip at site 18 in an 18 m mist net in primary forest along the Njo'o river (2.497915, 10.487032; 410 m) during the Great Dry Season (GDS).

Notes: The capture occurred under stable weather conditions (no strong wind, no rain, no moonlight) at mid-elevation. *Myotis dieteri* is a small vespertilionid (forearm < 37 mm) distinguished by its dark, "chocolate" brown, slightly woolly dorsal pelage and slightly paler ventral fur (Happold & Happold, 2013). Morphologically, it resembles *M. bocagii* but is notably smaller and possesses a unique wing membrane attachment at the base of the toes rather than the ankle (Happold & Happold, 2013). The species is believed to be associated with riverine systems and cave-roosting in forested landscapes. Its discovery in the Njo'o river basin suggests that *M. dieteri* may be more widely distributed across the Congolese-Lower Guinea forest interval than previously recognized, provided suitable riparian habitats are available. Acoustic

data from this individual revealed calls with a peak frequency of 76 kHz, frequency-modulated (FM) characteristic of the genus *Myotis*.

Myotis bocagii (W. C. H. Peters, 1870)
Bocage's Myotis

IUCN Red List status: Least Concern

New locality records: A single male of *Myotis bocagii* was captured during the fifth field trip at bootcamp site 20 in a 6 m mist net in secondary forest near a watercourse in Minkan Mengalé (2.506899, 10.73051; 510 m) during the GDS.

Notes: The individual escaped after initial identification, preventing full documentation. The capture occurred in rainy conditions at mid-elevation.

Genus *Pipistrellus* Kaup, 1829

Pipistrellus nanulus O. Thomas, 1904
Tiny Pipistrelle (Figure 3AA)

IUCN Red List status: Least Concern

New locality records: A total of 2 male *Pipistrellus nanulus* were captured during 2 field trips across 2 of the 20 sampling sites and throughout 2 seasons (GRS: 1; SRS: 1). Both individuals were recorded in primary forest: "camp couscous" on Dipikar Island (park's south sector: 2.26585, 9.91269; 27 m) and along a watercourse in the north sector of the park (2.733096, 10.308123; 202 m).

Notes: Captures occurred under light rain in 1 instance, and in dry conditions in the other at low altitude (27-202 m).

Pipistrellus sp. (Figure 3AB)

IUCN Red List status: Not yet assessed (Pending identification).

New locality records: A total of 2 males of *Pipistrellus* sp. were captured during the fifth field trip at bootcamp site 16 in human habitat (backyards and courtyards) in Nyamabandé (6 m mist net: 2.664099, 10.150193; 60 m; and 12 m mist net: 2.66339, 10.150161; 61 m) during the GDS.

Notes: Captures occurred under dry conditions at low altitude (60-61 m). The specimens exhibit the typical morphological suite of the genus *Pipistrellus*, including a small, slightly flattened skull and a simple, blunt tragus (Monadjem et al., 2020). However, the specific identity remains unresolved due to the high degree of morphological conservatism and cryptic diversity within the African *Pipistrellus/Neoromicia* complex.

The voucher specimens (registered as FM 500 and FM 501 in the original database) are currently characterized by dense, long-haired dorsal pelage that is distinctly bicolored: the hair bases are dark blackish-brown while the tips are a warm, burnished orange-brown (tawny). The ventral fur is slightly paler. The wing membranes (dactylopatagium and plagiopatagium) are uniform dark brown and semi-translucent, lacking any white posterior borders. The ears are short, rounded, and dark-pigmented, while the muzzle exhibits prominent glandular swellings

and sparse, fine vibrissae. Final taxonomic assignment is pending results from molecular barcoding (cyt-b and COI), as current morphological keys for the Lower Guinea forest region are insufficient to distinguish between several closely related congeners.

Genus *Neoromicia* Roberts, 1926

Neoromicia sp. (Figure 3AC)

IUCN Red List status: Not assessed (Pending identification).

New locality records: A single male of *Neoromicia* sp. was captured during the first field trip at bootcamp site 3 in a 6 m mist net in human habitat near fruit trees (*Carica papaya*, *Mangifera indica*, *Psidium guajava*) in Mvini village (2.373307, 10.10368; 93 m) during the Great Rainy Season (GRS).

Notes: The capture occurred under rainy conditions at low altitude, suggesting tolerance for wet weather. The individual was captured near fruit trees (*Carica papaya*, *Mangifera indica*, *Psidium guajava*), which may attract insect prey. The specimen lacks the distinct white wing margins seen in some *Neoromicia* species, possessing instead a uniform dark coloration.

The voucher specimen registered under FM 103, is well-preserved, and preliminary measurements (Forearm length: 34.9mm) place it within the mid-size range for the genus. Physically, the specimen is characterized by dense, woolly dorsal fur that is medium-brown with a slight grayish frost at the tips. The ears are relatively short and rounded with a slightly convex anterior margin, and the tragus is visible as a simple, blunt structure. The muzzle is broad with noticeable glandular pads, and the wing membranes are a consistent deep blackish-brown, appearing opaque compared to those of local *Pipistrellus*. Because recent systematic revisions have reassigned several *Neoromicia* species to the genus *Pseudoromicia* or *Laephotis* (Monadjem et al., 2020), this individual is being treated as *Neoromicia* sensu lato until barcoding analyses are completed. This molecular confirmation is essential to determine whether the specimen represents a known forest species or a potential extension of the range of a lineage more commonly associated with other types of habitats.

Genus *Pseudoromicia* Monadjem, Patterson, Webala & Demos, 2020

Pseudoromicia roseveari (Monadjem, Richards, Taylor and Stoffberg, 2013)

Rosevear's Serotine (Figure 3AD)

IUCN Red List status: Endangered

Previous distribution and range extension: Until recently, *Ps. roseveari* was considered endemic to the Upper Guinea forest zone, with records restricted to Mount Nimba (Liberia) and the Simandou Range (Guinea) (Monadjem et al., 2013). However, recent surveys have significantly expanded its known range into Central Africa. The species has been recorded in the Mbam Minkom Massif in central Cameroon (Grunwald et al., 2025) and within the continental rainforests of Equatorial Guinea (Torrent et al., 2025a). Our record from Campo-Ma'an National Park further confirms its presence in the coastal forests of South Cameroon, representing a southern range extension within the country.

New locality records: A single female *Pseudoromicia roseveari* was captured during the first field trip at bootcamp site 3 in a 12 m mist net in primary forest near Chinese bamboo in Mvini (2.367991, 10.109575; 70 m) during the Great Rainy Season (GRS). The individual was originally misidentified as *Pseudoromicia* cf. *brunnea* due to the overlapping dark chocolate-brown pelage characteristic of the "dark-winged" *Pseudoromicia* group. However, cyt-b analyses revealed a strong genetic proximity to *Ps. roseveari*.

Notes: This capture occurred under rainy conditions at low altitude. *Ps. roseveari* is characterized by a robust skull and broad snout relative to its congeners, with a total body length of approximately 89-91 mm and a forearm length of ~37 mm (Monadjem et al., 2013). Morphologically, it can be distinguished from *P. brunnea* by its larger size and specific craniodental features, including a braincase that rises more sharply above the rostrum (Monadjem et al., 2013).

As an Endangered species, its presence in Campo-Ma'an is of conservation significance. *Ps. roseveari* is believed to be a forest-dependent specialist, making it highly vulnerable to habitat fragmentation and loss (Monadjem et al., 2013). The species faces severe threats from deforestation driven by logging and agricultural expansion across the Lower Guinea rainforest (Grunwald et al., 2025; Torrent et al., 2025a). No acoustic data were obtained for this species during this survey, but previous studies suggest it prefers forest edges and riparian corridors for foraging (Monadjem et al., 2021).

Genus *Scotophilus* Leach, 1821

Scotophilus nux O. Thomas, 1904
Nut-colored Yellow Bat (Figure 3AE)

IUCN Red List status: Least Concern

New locality records: A total of 8 *Scotophilus nux*, including 4♀♀, 4♂♂ (including 1 juvenile male) were captured during 2 field trips, all at bootcamp site 1, and throughout 2 seasons (SDS: 5; GRS: 3). Individuals were recorded in 2 habitat types: secondary forest (6) and human habitat (2). Capture locations included secondary forest near a watercourse by Chinese bamboo in Nkoelon village (2.397567, 10.042823; 104 m) and ecolodge courtyards in Nkoelon (2.397096, 10.045225; 113 m).

Notes: Captures occurred under a wide range of weather conditions. Acoustic data showed short-duration FM calls (Dur ~ 2 ms).

Echolocation calls of recorded bat species

Acoustic parameters were characterized for 201 individuals representing 22 species (21 insectivorous and 1 frugivorous, *Rousettus aegyptiacus*), with sample sizes ranging from 1 individual (*Rhinolophus denti*, *Miniopterus inflatus*, *Kerivoula lanosa*, *K. phalaena*, *Myotis dieteri*) to 126 individuals (*Hipposideros* cf. *ruber*), these parameters are summarized in Table 2. High variability in peak frequency was observed in *Hipposideros* cf. *ruber* (SD = ±41.25 kHz), suggesting intraspecific variation potentially linked to sex, age, or cryptic lineage differences within the sampled population. Characteristic frequency values for *Rhinolophus landeri* (Fc ≈ 101,8 kHz) and *R. alcyone* (Fc ≈ 71,67 kHz) were consistent with published



Figure 3: Portraits of 31 species captured and photographed from CMNP and vicinity from August 2023 to February 2025: (A) *Casinonycteris campomaanensis*, (B) *Epomops franqueti*, (C) *Hypsignathus monstrosus*, (D) *Megaloglossus woermanni*, (E) *Myonycteris angolensis*, (F) *Myonycteris torquata*, (G) *Rousettus aegyptiacus*, (H) *Scotonycteris zenkeri*, (I) *Doryrhina cyclops*, (J) *Hipposideros beatus*, (K) *Hipposideros* cf. *ruber*, (L) *Rhinolophus alcyone*, (M) *Rhinolophus* cf. *blasii*, (N) *Rhinolophus* cf. *acrotis*, (O) *Rhinolophus denti*, (P) *Rhinolophus landeri*, (Q) *Miniopterus inflatus*, (R) *Nycteris arge*, (S) *Nycteris grandis*, (T) *Nycteris hispida*, (U) *Afronycteris nanus*, (V) *Glauconycteris alboguttata*, (W) *Glauconycteris* cf. *humeralis*, (X) *Kerivoula lanosa*, (Y) *Kerivoula phalaena*, (Z) *Myotis dieteri*, (AA) *Pipistrellus nanulus*, (AB) *Pipistrellus* sp., (AC) *Neoromicia* sp., (AD) *Pseudoromicia roseveari*, (AE) *Scotophilus nux*. ©Laurent Essome, Léger Offono and Franck Meyo

records for Central African populations (Monadjem et al., 2020). The preliminary CMNP call reference library, representing the first systematic acoustic documentation for this region, is available upon request from the corresponding author.

Genetics

We successfully sequenced the cytochrome b gene from 168 samples across 17 species. BLAST-N results, using default parameters (E-value < 0.05; query coverage >95%), suggested corrections for several morphological diagnoses with high nucleotide identities (96 - 99%). For instance, a specimen initially identified as *Pseudoromicia brunnea* (Collection No. FM156) matched *Pseudoromicia roseveari* with 95.59% identity (Accession No. MT777945). Similarly, *Rhinolophus fumigatus* (FM68) aligned to *Rhinolophus alcyone* with 98.76% identity (Accession No. PX550982), and *Rhinolophus landeri* (FM76) to *Rhinolophus denti* with 99.21% identity (Accession No. MN025578). Two *Rhinolophus alcyone* (FM161 and FM162) were aligned to *Rhinolophus landeri* (97.89 and 98.39% respectively) under the accession number PP942893. We also noted 1 *Hipposideros cf. ruber* (FM168) matching at 98.51% with *Hipposideros caffer* under the accession No. JQ956448, and *Miniopterus fraterculus* (FM38) to *Miniopterus inflatus* with 99.12% identity (Accession No. JQ956447). In addition, we noticed multiple *Epomops franqueti* specimens reassigned to *Epomophorus dobsonii* (FM94, 89.96%, Accession No. NC_046911) or *Myonycteris brachycephala* (FM81, 92.06%, Accession No. JX283222); due to the low degree of similarity (84–90%), caution is advised and further validation via nuclear markers would be necessary. We have therefore decided to retain them as *E. franqueti*.

These genetic refinements (representing ~10% of sequenced specimens) resolved cryptic diversity in morphologically conservative groups, such as Rhinolophidae and Vespertilionidae, and underscore the value of multiple lines of evidence for accurate species inventories in understudied regions. Maximum-likelihood phylogenetic trees based on cyt-b sequences from misidentified individuals, supplemented with BLAST-N reference sequences, and an excel spreadsheet with sample details for 6 species that have been genetically corrected are provided in the Supplementary support ([S2](#)), and detailed specimen data for all corrected and uncertain identifications are provided in Supplementary support ([S4](#)).

Species Richness and Abundance

Farms recorded the highest proportion of bats captured (31.2%), while secondary forest had fewer captures (20%). Species richness, diversity, and equitability were highest in primary forest (n = 23, H = 2.24 and J = 0.71). In contrast, farms showed lower richness and diversity (n = 15 and H = 1.78), although sampling completeness was the highest in this habitat (SC = 0.97).

Secondary forest displayed the strongest dominance pattern, driven by *H. cf. ruber* (D = 0.27), which accounted for 49.6% of captures in this habitat. Estimated richness based on rare species (singletons/doubletons) exceeded observed species for all habitat types. The Chao-1 estimator was greater in human-modified habitats (Chao-1 = 29) than in secondary forest (Chao-1 = 19.2) (Table 3).

Across seasons, the highest proportion of individuals was captured during the GDS (34.72%), with captures dominated by *H. cf. ruber* (32.71%). The SRS recorded fewer captures (15.84%) but exhibited the greatest evenness ($J = 0.77$).

Species richness and diversity were greatest during the GRS ($n = 22$, $H = 2.33$). Richness declined during both the SRS and SDS ($n=16$), and diversity was lowest during the SDS ($H = 1.93$). Sampling completeness was highest during the SDS ($SC=0.98$), which similar to the GDS, was characterized by dominance of *H. cf. ruber* ($D = 0.191$).

Estimated species richness based on rare species (singletons/doubletons) was greater than observed species in all seasons. The Chao-1 estimator was highest during the GRS (Chao-1 = 34) and lowest during the SDS (Chao-1 = 16.5) (Figure 4). In addition, these species exceeded observed richness for all habitat types: primary forest (Chao-1 = 30.2), human habitats (Chao-1 = 29), secondary forest (Chao-1 = 19.2), and farms (Chao-1 = 17.5) (Table 3).

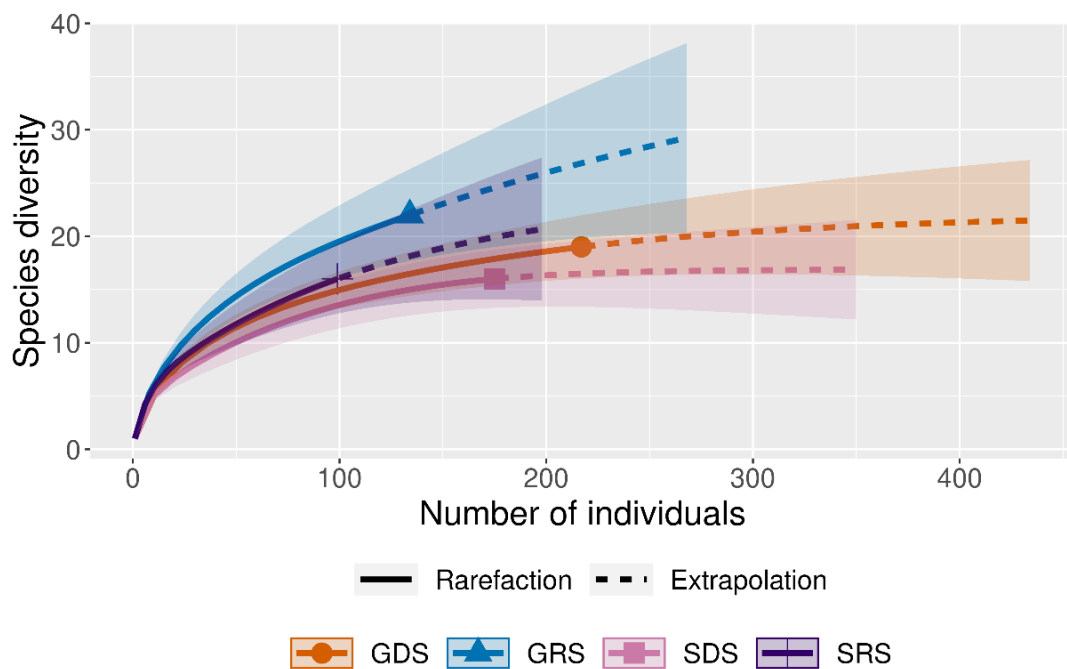


Figure 4: Sample size-based rarefaction and extrapolation (R/E) curves that include 95% confidence intervals for species richness ($q = 0$) showing abundance, Species richness and Diversity of bats according to seasons. Caption: **GDS:** Great Dry Season, **GRS:** Great Rainy Season, **SDS:** Short Dry Season, and **SRS:** Short Rainy Season.

Habitat types used by bats

We characterized bat habitat use across 4 habitat types, they were defined as follows: (1) primary forest (intact, undisturbed evergreen forest with dense canopy cover); (2) secondary forest (regenerating forest with open flyways and moderate anthropogenic disturbance); (3) farms (agricultural landscapes including cocoa, banana, rubber plantations, and palm groves); and (4) human habitats (built environments including villages, residential compounds, ecolodges, schools, and hospital grounds). Habitat-specific patterns, including species richness, abundance, key capture locations, and associations with fruit trees (*Annona muricata*, *Carica papaya*, *Cola acuminata*, *Dacryodes edulis*, *Garcinia kola*, *Mangifera indica*, *Psidium guajava*), are summarized in Table 4.

Table 2: Acoustic values of 21 collected and identified insectivorous and one frugivorous bat species from CMNP: Count= abundance; Frequencies values in kilohertz (kHz): Fppeak= Peak; Fc= characteristic; Fk= knee; Fmax= maximum; Fmin=minimum; Fmean=mean; dBmean= intensity in decibels; N= number of pulses emitted by the bat; Dur= duration of pulse in miliseconds (ms); Frequency Type: FM=Modulated Frequency, CF=Constancy Frequency.

Species	Count & sex	Type	Fppeak (kHz)				Fc (kHz)				Fk (kHz)			
			Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
Pteropodidae														
<i>Rousettus aegyptiacus</i>	5(4A, 1J) (1♀, 3♂)	FM	19	7,35	10	25	17	7,04	10	25	17	7,03	10	25
Hipposideridae														
<i>Doryrhina cyclops</i>	11 (7A, 2SA, 2J) (6♀, 5♂)	CF	57,27	1,01	56	59	57,18	1,99	55	62	57,55	2,21	55	63
<i>Hipposideros beatus</i>	7 (5A, 2J) (2♀, 5♂)	CF	119,57	23,15	69	136	130,43	9,57	120	142	132	10,15	120	144
<i>Hipposideros cf. ruber</i>	126 (119A, 24SA, 24J) (109♀, 47♂)	CF	122,25	41,25	6	213	139,52	9,96	69	153	142,23	10,5	68	156
Rhinolophidae														
<i>Rhinolophus alcyone</i>	9A (6♀, 3♂)	CF	71,67	10,27	67	99	71,22	10,07	67	98	71,11	10,13	66	98
<i>Rhinolophus cf. acrotis</i>	4(3A, 1SA) (2♀, 2♂)	CF	68,25	0,5	68	69	66,25	2,87	62	68	66	2,71	62	68
<i>Rhinolophus cf. blasii</i>	5(4A, 1J) (2♀, 3♂)	CF	94,2	14,11	69	102	93,8	14,43	68	101	93	13,98	68	100
<i>Rhinolophus denti</i>	1♂J	CF	71	-	71	71	69	-	69	69	69	-	69	69
<i>Rhinolophus landeri</i>	10(4A, 1SA, 5J) (5♀, 5♂)	CF	101,8	1,81	98	103	101	2,58	95	103	100,3	2,67	95	103
Nycteridae														
<i>Nycteris arge</i>	2♂A	FM	12	8,48	6	18	58,5	55,86	19	98	59	56,57	19	99
<i>Nycteris grandis</i>	1♂A	FM	18	-	18	18	-	-	-	-	-	-	-	-
Miniopteridae														
<i>Miniopterus inflatus</i>	1♂A	FM	53	-	53	53	61	-	61	61	65	-	65	65
Vespertilionidae														
<i>Afronycteris nanus</i>	2A (1♀, 1♂)	FM	41,5	36,06	16	67	-	-	-	-	-	-	-	-
<i>Glauconycteris alboguttata</i>	2♀ Adults	FM	36	1,41	35	37	40	4,24	37	43	45,5	4,95	42	49
** <i>Glauconycteris cf. humeralis</i>	5 (3♀, 2♂)	FM	43,2	13,31	23	59	40,2	11,03	26	57	43,6	12,78	26	62
<i>Kerivoula lanosa</i>	1♀ A	FM	115	-	115	115	151	-	151	151	235	-	235	235
<i>kerivoula phalaena</i>	1♂A	FM	107	-	107	107	125	-	125	125	147	-	147	147
** <i>Myotis dieteri</i>	1♂A	FM	76	-	76	76	38	-	38	38	79	-	79	79
<i>Neoromicia sp.</i>	1♂A	FM	51	-	51	51	57	-	57	57	56	-	56	56
<i>Pipistrellus nanulus</i>	1♂A	FM	37	-	37	37	33	-	33	33	38	-	38	38
<i>Pipistrellus sp.</i>	2♂A	FM	44	42,43	14	74	69	1,41	68	70	72	1,41	71	73
<i>Scotophilus nux</i>	3A (1♀, 2♂)	FM	43	2	41	45	40	2,94	37	43	42,25	2,5	39	45

Continued

Species	Count & sex	Type	Fmax (kHz)				Fmin (kHz)				Fmean (kHz)			
			Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
Pteropodidae														
<i>Rousettus aegyptiacus</i>	5(4A, 1J) (1♀, 3♂)	FM	17,4	7,27	10	25	16,8	7,05	10	25	17	7,04	10	25
Hipposideridae														
<i>Doryrhina cyclops</i>	11 (7A, 2SA, 2J) (6♀, 5♂)	CF	58,36	2,16	56	64	52,55	4,84	44	61	57,27	2,19	55	63
<i>Hipposideros beatus</i>	7 (5A, 2J) (2♀, 5♂)	CF	134,14	10,02	122	146	119,29	10,11	108	131	131	10,03	120	143
<i>Hipposideros cf. ruber</i>	126 (119A, 24SA, 24J) (109♀, 47♂)	CF	143,99	10,23	70	158	123,87	13,46	65	143	140,0 3	10,4	69	152
Rhinolophidae														
<i>Rhinolophus alcyone</i>	9A (6♀, 3♂)	CF	72,22	10,46	67	100	63,89	9,73	58	89	71,56	10,31	67	99
<i>Rhinolophus cf. acrotis</i>	4(3A, 1SA) (2♀, 2♂)	CF	67,25	2,87	63	69	58,5	4,43	53	63	66,25	2,87	62	68
<i>Rhinolophus cf. blasii</i>	5(4A, 1J) (2♀, 3♂)	CF	95,2	14,67	69	103	81	10,86	62	88	94,2	14,11	69	102
<i>Rhinolophus denti</i>	1♂J	CF	70	-	70	70	62	-	62	62	69	-	69	69
<i>Rhinolophus landeri</i>	10(4A, 1SA, 5J) (5♀, 5♂)	CF	102,6	2,55	97	105	89,4	4,57	84	98	101,1	2,6	95	103
Nycteridae														
<i>Nycteris arge</i>	2♂A	FM	60	55,15	21	99	55,5	54,45	17	94	57,5	54,45	19	96
<i>Nycteris grandis</i>	1♂A	FM	-	-	-	-	-	-	-	-	-	-	-	-
Miniopteridae														
<i>Miniopterus inflatus</i>	1♂A	FM	84	-	84	84	46	-	46	46	62	-	62	62
Vespertilionidae														
<i>Afronycteris nanus</i>	2A (1♀, 1♂)	FM	-	-	-	-	-	-	-	-	-	-	-	-
<i>Glauconycteris alboguttata</i>	2♀ Adults	FM	66	7,071	61	71	30	2,83	28	32	44	4,24	41	47
<i>Glauconycteris cf. humeralis</i>	5 (3♀, 2♂)	FM	68,4	27,88	27	98	37,4	11,35	21	53	47,6	16,2	24	69
<i>Kerivoula lanosa</i>	1♀ A	FM	235	-	235	235	99	-	99	99	170	-	170	170
<i>kerivoula phalaena</i>	1♂A	FM	154	-	154	154	106	-	106	106	130	-	130	130
<i>Myotis dieteri</i>	1♂A	FM	90	-	90	90	31	-	31	31	55	-	55	55
<i>Neoromicia sp.</i>	1♂A	FM	80	-	80	80	49	-	49	49	60	-	60	60
<i>Pipistrellus nanulus</i>	1♂A	FM	81	.	81	81	32	.	32	32	48	.	48	48
<i>Pipistrellus sp.</i>	2♂A	FM	101,5	13,43	92	111	66	2,83	64	68	75,5	4,95	72	79
<i>Scotophilus nux</i>	3A (1♀, 2♂)	FM	72,25	6,994	63	79	38	2,16	35	40	49,25	2,87	47	53

Continued

Species	Count & sex	Type	dBmean				N				Dur (ms)			
			Mean	SD	Min	Max	Mean	SD	Min	Max	Mean	SD	Min	Max
Pteropodidae														
<i>Rousettus aegyptiacus</i>	5(4A, 1J) (1♀, 3♂)	FM	-35,75	16,88	-49	-11	3,4	2,19	1	7	3,8	1,3	3	6
Hipposideridae														
<i>Doryrhina cyclops</i>	11 (7A, 2SA, 2J) (6♀, 5♂)	CF	-16,73	9,68	-36	-4	12,45	9,66	1	29	17,91	4,87	11	27
<i>Hipposideros beatus</i>	7 (5A, 2J) (2♀, 5♂)	CF	-32,71	11,61	-50	-18	23,43	10,83	10	40	5,29	1,11	4	7
<i>Hipposideros cf. ruber</i>	126 (119A, 24SA, 24J) (109♀, 47♂)	CF	-41,47	8,31	-57	-15	17,01	11,38	2	52	5,01	3,72	3	45
Rhinolophidae														
<i>Rhinolophus alcyone</i>	9A (6♀, 3♂)	CF	-15,67	8,79	-28	-3	7	3,04	2	11	73	23,72	31	106
<i>Rhinolophus cf. acrotis</i>	4(3A, 1SA) (2♀, 2♂)	CF	-17	15,03	-37	-2	5,75	2,63	2	8	67,75	13,82	57	88
<i>Rhinolophus cf. blasii</i>	5(4A, 1J) (2♀, 3♂)	CF	-10	3,94	-14	-4	7	5,96	2	17	62	18,91	37	89
<i>Rhinolophus denti</i>	1♂J	CF	-28	-	-28	-28	40	-	40	40	9	-	9	9
<i>Rhinolophus landeri</i>	10(4A, 1SA, 5J) (5♀, 5♂)	CF	-20,1	9,39	-32	-7	9,1	3,54	4	17	51,1	28,58	24	107
Nycteridae														
<i>Nycteris arge</i>	2♂A	FM	-47	1,41	-48	-46	14,5	14,85	4	25	7	4,24	4	10
<i>Nycteris grandis</i>	1♂A	FM	-31	-	-31	-31	-	-	-	-	-	-	-	-
Miniopteridae														
<i>Miniopterus inflatus</i>	1♂A	FM	-17	-	-17	-17	26	-	26	26	4	-	4	4
Vespertilionidae														
<i>Afronycteris nanus</i>	2A (1♀, 1♂)	FM	-23	29,7	-44	-2	-	-	-	-	-	-	-	-
<i>Glauconycteris alboguttata</i>	2♀ A	FM	-14,5	7,79	-20	-9	9	1,41	8	10	2,5	0,71	2	3
<i>Glauconycteris cf. humeralis</i>	5 (3♀, 2♂)	FM	-17,2	7,29	-29	-11	6	5,1	2	14	3	1,22	2	5
<i>Kerivoula lanosa</i>	1♀ A	FM	-37	-	-37	-37	1	-	1	1	2	-	2	2
<i>kerivoula phalaena</i>	1♂A	FM	-44	-	-44	-44	3	-	3	3	3	-	3	3
<i>Myotis dieteri</i>	1♂A	FM	-16	-	-16	-16	3	-	3	3	5	-	5	5
<i>Neoromicia sp.</i>	1♂A	FM	-35	-	-35	-35	4	-	4	4	3	.	3	3
<i>Pipistrellus nanulus</i>	1♂A	FM	-5	-	-5	-5	8	-	8	8	3	-	3	3
<i>Pipistrellus sp.</i>	2♂A	FM	-32,5	14,85	-43	-22	4	4,24	1	7	3	0	3	3
<i>Scotophilus nux</i>	3A (1♀, 2♂)	FM	-11,33	10,15	-23	-5	9,75	7,76	2	20	2	0	2	2

Table 3 : Abundance, Species richness and Diversity of bats according to habitat types

Habitat	Abundance	Richness	Shannon	Simpson	Evenness J	Dominance_D	Chao-1	SC
Primary forest	140	23	2.24	0.796	0.714	0.204	30.2	0.936
Secondary forest	125	18	1.97	0.729	0.683	0.271	19.2	0.968
Human habitat	165	20	1.93	0.792	0.646	0.208	29	0.94
Farms	195	15	1.78	0.766	0.658	0.234	17.5	0.974

Primary forest is characterized by dense evergreen canopies, watercourses, and minimal disturbance. Dominant species included *Hipposideros cf. ruber* (58 individuals, 41%) and *Myonycteris torquata* (14 individuals), along with several species captured exclusively in this habitat, including *Casinycteris campomaanensis*, *Nycteris arge*, *Miniopterus inflatus*, *Myotis dieteri*, *Kerivoula phalaena*, *Pipistrellus nanulus*, and *Pseudoromicia roseveari*. Capture sites included watercourses, forest galleries, and areas within and around Chinese bamboo. Frugivorous bats, including *Epomops franqueti* (10 individuals) and *Scotonycteris zenkeri* (9 individuals), were frequently captured near fruit trees (*Dacryodes edulis*, *Mangifera indica*). Chao-1 estimated 30.2 species (SC = 0.94), suggesting considerable unobserved richness in this habitat so, indicating moderate sampling completeness.

Secondary forest, characterized by regenerating vegetation, open flyways, and moderate disturbance, had the lowest abundance (n=125, 20%) but moderate richness (18 species). *Hipposideros cf. ruber* dominated captures, along with *Scotophilus nux* (6 individuals) and *Rhinolophus landeri* (6 individuals). Capture sites included clearings, watercourses, and areas near Chinese bamboo, with *E. franqueti* (11 individuals) and *M. torquata* (3 individuals) associated with fruit trees (*Carica papaya*, *Psidium guajava*). Chao-1 estimated 19.2 species (SC=0.96), suggesting minimal unobserved richness, then indicating high sampling completeness.

Farms, encompassing cocoa, banana, and rubber plantations, recorded the highest abundance (n=195, 31.2%) but lower richness (15 species, H'=1.78). Frugivorous bats dominated, with *Megaloglossus woermanni* (74 individuals, 38%) and *E. franqueti* (41 individuals) captured near fruit trees (*Annona muricata*, *Carica papaya*, *Mangifera indica*, *Psidium guajava*) in cocoa and banana plantations. Other species included *Rhinolophus cf. blasii* (2 individuals) and *Afronycteris nanus* (1 individual) in banana farms. Capture sites included watercourses in forest pockets and palm groves. Chao-1 estimated 17.5 species (SC=0.97), indicating high sampling completeness.

Human habitats, including villages, ecolodges, and backyards, supported 18 species (n=165, 26%). *Rousettus aegyptiacus* (48 individuals, 29%) and *M. woermanni* (46 individuals) were dominant, captured near fruit trees (*Cola acuminata*, *Garcinia kola*, *Mangifera indica*) and anthropogenic structures. Notable records included 1 individual of *Myonycteris angolensis* and *Pseudoromicia roseveari*. Chao-1 estimated 29 species (SC=0.94), suggesting likely unobserved diversity, then indicating moderate sampling completeness.

Table 4: Habitat characteristics for bat associations (all coordinates are given in decimal degrees)

Habitat Type	Most abundant species (*Dominant species)	Capture sites	Environmental features	Vegetation and trees	Altitude range (m)
Primary Forest	<i>*H. cf. ruber</i> , <i>M. torquata</i> , <i>R. aegyptiacus</i>	<ul style="list-style-type: none"> - Cave - Chinese bamboo - Clearing - Forest (“camp couscous”, gallery over Otong Mekok watercourse, rocky forest) - Swamp - Uninhabited ecolodge ([2.36788, 10.325336, 388m]) - Watercourses (Dounba’andou, grand Medibane, Manebingang, petit Medibane, Ntebe zok, Ongat, Otong Mekok [2.541429, 10.485057], and others) - Waterpoints - River (mangrove Biwomé, Njo’o [2.51331, 10.731341]) 	Dense evergreen canopy, watercourses and low disturbance	<i>Cola acuminata</i> , <i>Dacryodes edulis</i> , <i>Garcinia kola</i> , <i>Mangifera indica</i> ,	27-537
Secondary Forest	<i>H. cf. ruber</i> , <i>E. franqueti</i> , <i>R. aegyptiacus</i> , <i>*D. cyclops</i>	<ul style="list-style-type: none"> - Backyards and courtyards of houses <ul style="list-style-type: none"> - Bridge - Cave - Chinese bamboo - Clearing - Farms - Forest - Picarthian cave - Swamp - Uninhabited ecolodge ([2.287161, 9.950594, 36 m]) - Watercourses (Awomo [2.769491, 10.656395], Bitandé, and other) - Waterpoints (Tenga Massila and others) - Farms (banana, cassava, cocoa) 	Regenerating vegetation, open flyways; moderate disturbance	<i>Artocarpus altilis</i> , <i>Carica papaya</i> , <i>Psidium guajava</i>	33-667
Farms	<i>R. aegyptiacus</i> , <i>*M. woermanni</i> , <i>E. franqueti</i>	<ul style="list-style-type: none"> - HEVECAM [2.671364, 10.019063], <ul style="list-style-type: none"> - Palm grove - Rubber plantation (watercourse in forest pocket) 	Cocoa/banana plantations, watercourses; moderate disturbance	<i>Annona muricata</i> , <i>Carica papaya</i> , <i>Mangifera indica</i>	29-571

Human Habitat	<i>M. woermanni</i> , <i>E. franqueti</i> , <i>H. cf. ruber</i> , <i>*R. aegyptiacus</i>	- Backyards and courtyards of houses	Backyards, ecolodges, fruit trees, houses, opened canopy; high disturbance	<i>Annona muricata</i> , <i>Carica papaya</i> , <i>Cola acuminata</i> , <i>Garcinia kola</i> , <i>Dacryodes edulis</i> , <i>Mangifera indica</i> , <i>Psidium guajava</i>	36-634
		- Bridge - CAMVERT entry gate - Chinese bamboo - Ecolodge courtyards - Ecolodge roof - Hospital backyard - House roof - Near fruit trees - Nozzle - School			

Bat assemblages across habitats and seasons

ANOSIM ($R = 0.4041$, $P = 0.0023$) and PERMANOVA ($F = 2.528$, $P = 0.0019$) with 9999 permutations confirmed significant differences in bat assemblages across habitat-season combinations. The moderate R and F values indicate notable but not complete separation in species composition. The NMDS ordination (stress = 0.2337) visualized patterns in bat assemblages across habitat and season (Figure 5). Primary and secondary forest sites sampled during the GRS and GDS formed a distinct cluster. Human habitats and farms grouped more closely together forming a second cluster. Some overlap was observed between and forest and human-modified habitats (Figure 5).

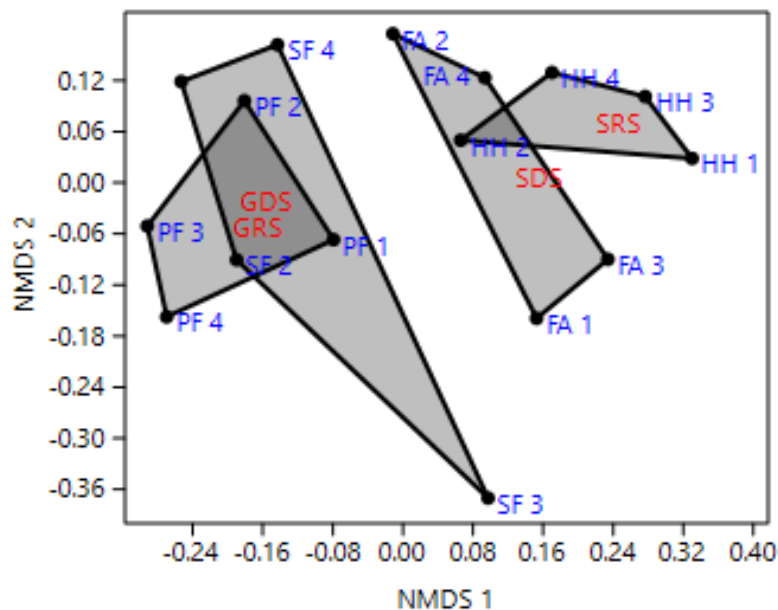


Figure 5: Non-metric Multidimensional Scaling (NMDS) ordination plot showing bat assemblages across habitat-season combinations. Points represent sampling sites, with red color indicating seasons (SDS, GRS, SRS, GDS) and shapes indicating habitats (primary forest, secondary forest, human habitat, farms).

Species contribution in overall dissimilarity

The SIMPER analysis quantified species contribution to community dissimilarity between the different habitat types and seasons, and we noted an overall dissimilarity of 71.33% (Table 5). The majority of the dissimilarity (65%) was driven by a small group of dominant species,

including *Hipposideros cf. ruber*, *Miniopterus inflatus*, *Megaloglossus woermanni*, and *Rousettus aegyptiacus*. A second group of species, *Epomops franqueti*, *Myonycteris torquata*, *Scotonycteris zenkeri*, *Doryrhina cyclops*, *Rhinolophus landeri*, *Hipposideros beatus*, *Scotophilus nux*, *Rhinolophus alcyone*, *Nycteris grandis*, *Hypsignatus monstrosus*, and *Rhinolophus cf. blasii*, contributed 28.60% to the dissimilarity. The remaining species *Rhinolophus cf. acrotis*, *Glauconycteris cf. humeralis*, *Pipistrellus nanulus*, *Glauconycteris alboguttata*, *Pipistrellus sp.*, *Nycteris arge*, *Afronycteris nanus*, *Rhinolophus denti*, *Neoromicia sp.*, *Myotis bocagii*, *Pseudoromicia roseveari*, *Casinycteris campomaanensis*, *Kerivoula lanosa*, *Nycteris hispida*, *Myonycteris angolensis*, and *Kerivoula phalaena* contributed a combined 6.30%.

Table 5: Percentages of contributions (SIMPER) of species to the dissimilarity according to habitat-season combination patterns.

Species	Av. dissim	Contrib. %	Cumulative %
<i>Hipposideros cf. ruber</i>	12.87	18.05	18.05
<i>Miniopterus inflatus</i>	12.68	17.78	35.82
<i>Megaloglossus woermanni</i>	11.74	16.47	52.29
<i>Rousettus aegyptiacus</i>	9.009	12.63	64.92
<i>Epomops franqueti</i>	6.365	8.924	73.84
<i>Myonycteris torquata</i>	3.572	5.008	78.85
<i>Scotonycteris zenkeri</i>	1.777	2.492	81.34
<i>Doryrhina cyclops</i>	1.473	2.065	83.41
<i>Rhinolophus landeri</i>	1.435	2.012	85.42
<i>Hipposideros beatus</i>	1.333	1.868	87.29
<i>Scotophilus nux</i>	1.031	1.445	88.73
<i>Rhinolophus alcyone</i>	1.009	1.415	90.15
<i>Nycteris grandis</i>	0.8815	1.236	91.38
<i>Hypsignatus monstrosus</i>	0.7979	1.119	92.5
<i>Rhinolophus cf. blasii</i>	0.7285	1.021	93.52
<i>Rhinolophus cf. acrotis</i>	0.6969	0.9771	94.5
<i>Glauconycteris cf. humeralis</i>	0.6419	0.9	95.4
<i>Pipistrellus nanulus</i>	0.3566	0.4999	95.9
<i>Glauconycteris alboguttata</i>	0.3404	0.4773	96.38
<i>Pipistrellus sp.</i>	0.339	0.4753	96.85
<i>Nycteris arge</i>	0.2987	0.4187	97.27
<i>Afronycteris nanus</i>	0.2825	0.3961	97.67
<i>Rhinolophus denti</i>	0.218	0.3056	97.97
<i>Neoromicia sp.</i>	0.218	0.3056	98.28
<i>Myotis bocagii</i>	0.1972	0.2765	98.56
<i>Pseudoromicia roseveari</i>	0.1798	0.252	98.81
<i>Casinycteris campomaanensis</i>	0.1768	0.2479	99.06
<i>Kerivoula lanosa</i>	0.1596	0.2237	99.28
<i>Nycteris hispida</i>	0.1449	0.2031	99.48
<i>Myonycteris angolensis</i>	0.1251	0.1754	99.66
<i>Kerivoula phalaena</i>	0.1219	0.1708	99.83
<i>Myotis dieteri</i>	0.1219	0.1708	100

Discussion

CMNP as a biodiversity hotspot in the Guineo-Congolian Rainforest

Campo-Ma'an National Park (CMNP) supports a remarkable bat diversity, with 32 species across 20 genera and 6 families, representing approximately 27% of Cameroon's known chiropteran fauna (118 species; Van Cakenberghe & Seamark, 2025). This richness underscores CMNP's role as a critical biodiversity reservoir within the Guineo-Congolian rainforest, aligning with regional assessments (Bakwo Fils, 2009; Atagana et al., 2021).

This study documented 2 confirmed first country records for Cameroon: *Rhinolophus denti* (genetically confirmed via cyt-b) and *Myotis dieteri*, the latter also representing the first documented occurrence of this species within any protected area globally (Montauban et al., 2025). Three additional potential first country records, pending further genetic confirmation, include *R. cf. blasii*, *R. cf. acrotis*, and *Glauconycteris cf. humeralis*.

Notable records also include *Casinycteris campomaanensis* (Data Deficient), from which only a few specimens are known, including the type specimen collected near CMNP (Hassanin, 2014). Additional records of *C. campomaanensis* have been reported from Nigeria (Tanshi et al., 2019), possibly the Republic of the Congo, and recently confirmed in Equatorial Guinea (Torrent et al., 2025a), underscoring its rarity and restricted distribution. Additional species of conservation concern include *Scotonycteris zenkeri* (Near Threatened; IUCN, 2025) and *Pseudoromicia roseveari* (Endangered; Monadjem, 2017), the latter confirmed genetically and representing a southern range extension within Cameroon (previously recorded in the Mbam Minkom Massif by Grunwald et al., 2025). These records further emphasize the conservation significance of CMNP as a critical refuge for rare, threatened, and data-deficient bat species.

Several additional taxa, including *Miniopterus inflatus* and *Glauconycteris cf. humeralis*, require further taxonomic assessment to clarify their identity and conservation status. Montauban et al. (2025) noted that 28 bat species, including 5 threatened and 15 data-deficient taxa (including *Myotis dieteri*) remain unrecorded in sub-Saharan Africa's protected areas, with Central African parks, such as CMNP, particularly understudied. The absence of some of these species in our dataset likely reflects incomplete sampling and emphasizes the need for expanded temporal and methodological coverage to fully document CMNP's bat fauna and address continental gaps in bat records.

Bat species inventory and acoustic monitoring efficacy

The combined use of mist nets, harp traps, and acoustic monitoring facilitated the capture and recording of both frugivorous and elusive insectivorous taxa. This aligns with recommendations for complementary sampling approaches in tropical systems (MacSwiney et al. (2008); Walters et al. 2013). Such integrative strategies are particularly valuable in understudied regions of Africa, such as the Campo locality, as highlighted by Tanshi et al. (2019).

Active acoustic monitoring using the AnaBat Walkabout was essential for characterizing echolocation calls of captured individuals. The acoustics data generated for 22 species (21 insectivorous, 1 frugivorous) provided a foundation for future non-invasive monitoring (Hintze et al., 2021). The recorded species exhibited call types consistent with their known foraging

ecology: Rhinolophidae and Hipposideridae produce constant frequency (CF) calls typically associated with cluttered forest environments, while Nycteridae, Vespertilionidae, and *Rousettus aegyptiacus* produce frequency-modulated (FM) calls suited to more open habitats (Monadjem, 2020). We noted high variability in *Hipposideros cf. ruber* peak frequency ($SD = \pm 41.25$ kHz) which may suggest intraspecific variation, possibly due to sex, age, or environmental adaptation, warranting further study (Brigham et al., 1989; Russo et al., 2001; Jones & Siemers, 2011). The failure of our triple-high mist net system limited canopy sampling, potentially underestimating canopy-dwelling species (Kunz & Parsons, 2009). The preliminary CMNP acoustic reference library, available upon request from the corresponding author, provides a foundation for future non-invasive monitoring of rare and conservation concern species, contributing to regional conservation efforts (Walters et al., 2013).

Seasonal and habitat variation in diversity and abundance

Bat diversity and abundance varied significantly across habitats and seasons, likely reflecting ecological niches and resources availability. Primary forests exhibited the highest species richness (23 species, $H' = 2.24$, $J' = 0.71$), consistent with findings from the Dja Biosphere Reserve, where higher bat species richness was recorded in primary forests (17 species) (Atagana et al., 2021). The elevated richness recorded in CMNP's primary forests, together with findings from Atagana et al. (2021) and Waghiiwimbom et al. (2020), who also reported higher bat diversity in less disturbed habitats in Cameroon's Centre Region, reinforces the critical role of primary forests as biodiversity reservoirs for bats and highlights their importance as a conservation priority. In addition, primary forests hosted several rare species captured exclusively in this habitat, including *M. dieteri* and *N. arge*, likely due to dense vegetation and stable microclimatic conditions (Kunz et al., 2011). Secondary forests supported moderate species richness (18 species) but were dominated by *H. cf. ruber* ($D = 0.27$), suggesting that this species may be particularly well adapted to regenerating habitats (Vleut et al., 2013; Webala et al., 2019). Farms showed the lowest richness (15 species, $H' = 1.78$) but high abundance (31.2% of captures), largely driven by frugivorous generalists like *M. woermanni* and *E. franqueti*, which exploit fruit trees such as *Mangifera indica* and *Carica papaya* in agricultural landscapes. Human habitats hosted adaptable species like *R. aegyptiacus* and *A. nanus*, indicating the supplementary roles of that anthropogenic landscapes can play for some bat species (Atagana et al., 2021). In CMNP, species richness in human habitats exceeded that observed in farms, contrasting patterns reported by Atagana et al. (2021). The difference suggests that human habitats in CMNP may provide more ecological niches or resources for certain bat species. This variation underscores the influence of site-specific factors, such as habitat structure and differing levels of disturbance, that influence bat community composition. Further research is needed to elucidate the mechanisms driving these patterns and to inform tailored conservation strategies for bat populations across diverse land-use types in Cameroon.

Seasonally, the Great Dry Season (GDS) recorded the highest abundance (34.72%), likely due to increased insect availability, while the Great Rainy Season (GRS) showed the highest richness (22 species, $H' = 2.33$), possibly reflecting peak fruit and insect availability (Klingbeil & Willig, 2010). The Small Rainy Season (SRS) had the lowest capture rate (15.84%) but the highest evenness ($J' = 0.77$), indicating a more equitable distribution of individuals among species. Comparing seasonal patterns with previous studies, Klingbeil & Willig (2010) reported

similar bat diversity between wet and dry seasons in Amazonian rainforest near Iquitos, Peru. Our results partially support this pattern: richness was comparable between the SRS and SDS (16 species each). However, we observed greater differences between the GRS (22 species) and GDS (19 species), suggesting that seasonal effects on bat communities may be more pronounced in the four-season equatorial climate of CMNP compared to the 2-season system studied in Amazonia. The observed differences may reflect regional difference in ecological dynamics between Africa and South America, as well as seasonal structure, we distinguished 4 seasons while they recorded 2.

Environmental factors influencing species distributions

Habitat type and season interacted to shape bat assemblage structure in CMNP. Forest habitats (primary and secondary) supported distinct communities compared to human-modified landscapes (farms and human habitats), which shared generalist species. This pattern reflects the ecological flexibility of dominant species such as *H. cf. ruber*, *M. woermanni*, and *R. aegyptiacus*, which were the primary drivers of community dissimilarity across habitat-season combinations.

Environmental factors including vegetation structure, water proximity, and fruit tree availability likely underlie these patterns (Voigt & Kingston, 2016). Primary forests supported insectivorous species such as *R. landeri*, while farms attracted frugivores like *E. franqueti* that exploit cultivated fruit trees. The moderate but significant habitat-season effects suggest that additional unmeasured factors, such as microclimate, specific fruit availability for frugivores, or prey availability for insectivores, may also influence bat distributions (Ramos Pereira et al., 2010). Furthermore, relationships between landscape structure and bat communities may be season-specific, warranting long-term monitoring to capture interannual variation (Klingbeil & Willig, 2010).

Despite high sampling completeness across most habitats and seasons, estimated species richness in human habitats exceeded observed richness, suggesting that additional rare or elusive species may remain undetected in anthropogenic environments (Chao et al., 2014).

Characterization of habitat types used by bats

Bat habitat use in CMNP reflected distinct ecological niches shaped by vegetation structure, fruit tree availability, water proximity, and disturbance levels (Table 4). Primary forests supported the highest species richness and were the exclusive capture habitat for several rare, potentially forest-dependent species, including *K. phalaena*, *M. dieteri*, *N. arge*, and *P. nanulus* (T. Kunz & Parsons, 2009; Meyer et al., 2004). The structural complexity of primary forests (dense canopy cover, abundant watercourses, and minimal disturbance), likely provides essential roosting and foraging resources for these species. Frugivorous bats such as *M. torquata* were also well-represented in primary forest, attracted by native fruit trees (*Cola acuminata*, *Dacryodes edulis*, *Mangifera indica*), underscoring the role of intact forests in maintaining seed dispersal networks (Kunz et al., 2011; Happold & Happold, 2013). Secondary forests supported moderate diversity, dominated by generalist species such as *H. cf. ruber*, *E. franqueti*, and *R. aegyptiacus* that thrive near watercourses and cultivated fruit trees. The broad elevational range of captures (33 - 667 m) suggests adaptability to varied conditions, consistent with patterns observed in other African forests (Webala et al., 2019). Farms exhibited the

highest abundance but lowest species richness, driven by frugivorous generalists (*M. woermanni*, *E. franqueti*) exploiting cultivated fruit trees in cocoa and banana plantations. This pattern (high abundance, low diversity, frugivore dominance) aligns with findings from other Central African, specifically Cameroon agroecosystems (Atagana et al., 2021) and highlights the importance of fruit trees in structuring bat communities in agricultural landscapes. Human habitats supported a diverse assemblage despite high disturbance levels. Species such as *R. aegyptiacus*, *M. woermanni*, and several Rhinolophidae were frequently captured near anthropogenic structures, reflecting tolerance for disturbed landscapes and the supplementary foraging opportunities provided by fruit trees maintained near houses (Atagana et al., 2021).

These findings emphasize that maintaining habitat heterogeneity (including primary forest cores, regenerating secondary forests, and fruit tree-rich agricultural mosaics) is essential for conserving bat diversity across the CMNP landscape.

Conservation challenges and opportunities

CMNP faces significant threats from deforestation, agro-industrial expansion (e.g., HEVECAM, CAMVERT), and infrastructure development, which fragment habitats and disrupt bat foraging and roosting (Engolo et al., 2024). These pressures align with broader challenges in African tropical forests, where bats are often overlooked in conservation planning (Bakwo Fils, 2009; Voigt & Kingston, 2016).

Our inventory documented several species of conservation concern, including *C. campomaanensis* and *M. dieteri* (Data Deficient), *S. zenkeri* (Near Threatened), and *Ps. roseveari* (Endangered). Montauban et al. (2025) emphasized that understudied protected areas like CMNP may harbor additional unrecorded threatened or data-deficient species, and the potential for undetected species suggested by our Chao-1 estimates supports this view. Expanded surveys with increased temporal and spatial coverage are needed to fully document CMNP's bat fauna.

Several taxa collected during this study (including *G. cf. humeralis*, *M. inflatus*, *Neoromicia sp.*, and *Pipistrellus sp.*) remain taxonomically unresolved (Not Assessed by IUCN). Integrative approaches combining morphology, acoustics, and multi-locus genetic analyses are essential to clarify their identity and assess their relationships and conservation requirements (Patterson et al., 2020; Montauban et al., 2025).

Future research should employ complementary approaches to improve species detection and inform conservation planning. Species distribution modeling (e.g., MaxEnt) could predict habitat suitability for rare species such as *Ps. roseveari* and identify key environmental drivers including watercourses, fruit tree density, and vegetation structure. Passive acoustic monitoring (e.g., using passive SM4BAT FS detectors) could increase detection of rare and elusive species that may be missed by capture-based methods alone (Hintze et al., 2021).

Several practical conservation measures could enhance bat populations in CMNP. Integrating bat-friendly practices into the park's management plan (such as designating roosting sites, maintaining forest corridors, and protecting primary forests) would directly benefit forest-dependent species (Frick et al., 2020; Montauban et al., 2025). Promoting fruit tree agroforestry (e.g., *Mangifera indica*, *Psidium guajava*) in surrounding agricultural landscapes could support frugivorous bat populations while providing sustainable livelihoods for local communities (Fahr & Kalko, 2011). Community engagement through ecotourism and environmental

education can further promote bat conservation by highlighting their ecosystem services, including pollination, seed dispersal, and pest control (Kunz et al., 2011; UNESCO, 2018).

Genetic insights and taxonomic refinements and implications

Cytochrome b sequencing of 168 tissue samples proved essential for resolving taxonomic uncertainties, with BLAST-N analyses correcting approximately 10% of field identifications, mainly within morphologically conservative families. Within Rhinolophidae, a specimen first identified as *Rhinolophus landeri* was reassigned to *R. denti* (99.21% identity), representing the first genetically confirmed country record for this species in Cameroon (although *R. cf. denti* was previously recorded morphologically at one locality). Similarly, *R. fumigatus* aligned with *R. alcyone* (98.76%), while 2 specimens of *R. alcyone* were reassigned to *R. landeri* (97.89 - 98.39%). These bidirectional misidentifications reflect extensive noseleaf morphology overlap among African rhinolophids (Dool et al., 2016; Demos et al., 2019). Within Vespertilionidae, *Pseudoromicia brunnea* was corrected to the Endangered *Ps. roseveari* (95.59% identity), confirming this species' presence in CMNP and extending its known range into the Lower Guinea forest block (Grunwald et al., 2025; Torrent et al., 2025a). Additionally, *Miniopterus fraterculus* was reassigned to *M. inflatus* (99.12% identity), consistent with the morphological conservatism characterizing this genus (Happold & Happold, 2013).

Low identity scores (84 - 92%) for *Epomops franqueti* specimens likely reflect incomplete reference databases rather than genuine misidentification, as morphological features clearly supported field assignments. We retained these specimens as *E. franqueti* pending improved sequence coverage of Afrotropical pteropodids (Hassanin et al., 2015). Several taxa remain provisionally identified: *Glauconycteris cf. humeralis*, *Neoromicia sp.*, and *Pipistrellus sp.* each require multi-locus nuclear data for definitive assignment (Hassanin et al., 2018; Monadjem, Shapiro, et al., 2020).

The ~10% correction rate underscores that morphology-based identification alone underestimates diversity and can result in misidentification of conservation-priority species. The *Hipposideros cf. ruber/caffer* complex exemplifies these challenges. High acoustic variability in peak frequency (SD = ± 41.25 kHz) suggests intraspecific variation or cryptic diversity, and BLAST-N results revealed 1 specimen matching *H. caffer* at 98.51% identity rather than *H. ruber*. This finding aligns with Monadjem et al. (2013), who demonstrated that *H. ruber* and *H. caffer* are frequently confused due to overlapping morphology and sympatric distributions across Africa. More recently, Patterson et al. (2020) used multi-locus sequences to document four different species-level clades within what is called *Hipposideros ruber* and four within *H. caffer*. Given this uncertainty, we retain the "cf." qualifier for all 172 *Hipposideros* individuals pending comprehensive integrative revision combining morphology, echolocation acoustics, and multi-locus nuclear markers (Demos et al., 2019; Patterson et al., 2020). Future studies should incorporate nuclear data to clarify species boundaries within this complex and determine whether CMNP hosts 1 variable population or multiple sympatric cryptic species.

Author contribution

FPMO: investigation, methodology, data curation, formal analysis, visualization, writing-original draft and editing;

PAN: supervision, resources, data curation, writing-critical review and editing;

ALG: methodology, resources, visualization, writing-critical review and editing;

TCD: formal analysis, resources, writing-review and editing

LEN: investigation, writing-review and editing;

ERH: formal analysis, writing-review and editing;

BDP: supervision, resources, writing-critical review and editing;

EMBF: supervision, resources, formal analysis, writing-critical review and editing.

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